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OM protein - protein search, using sw model

Run on: October 2, 2000, 17:32:35 ; Search time 107.24 Seconds
(without alignments)
1.876 Million cell updates/sec

Title: US-09-142-613-2
Perfect score: 62
Sequence: 1 KSGXSXPSPCT 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 164575 seqs, 16761186 residues

Total number of hits satisfying chosen parameters: 164575

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: Issued_Patents_AA:*
2: /cgn2_6/ptodata/1/1aa/5A.COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/5B.COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/6.COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/6CTMS.COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/6Cfct1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	58	93.5	31	2	US-08-244-951A-4
2	58	93.5	34	2	US-08-602-264A-10
3	58	93.5	34	3	US-08-461-018A-10
4	58	93.5	67	2	US-08-244-951A-1
5	58	93.5	67	3	US-08-403-917A-1
6	58	93.5	67	3	US-08-776-404B-1
7	58	93.5	106	3	US-08-666-360-1
8	58	93.5	112	3	US-08-159-969-2
9	58	93.5	351	1	US-08-726-306A-17
10	58	93.5	352	2	US-08-244-951A-10
11	58	93.5	391	2	US-08-389-011-23
12	58	93.5	391	2	US-08-403-917A-23
13	58	93.5	391	2	US-08-403-917A-23
14	56	90.3	27	2	US-08-244-951A-5
15	39	62.9	252	3	US-09-057-088-8
16	39	62.9	427	1	US-07-956-700B-3
17	39	62.9	427	1	US-08-476-537-3
18	39	62.9	427	1	US-08-485-607-3
19	39	62.9	427	1	US-08-475-879-3
20	39	62.9	427	1	US-08-611-107-6
21	39	62.9	447	2	US-08-422-560A-6
22	39	62.9	160	2	US-08-726-306A-35
23	37	59.7	455	2	US-08-035-928-2
24	37	59.7	545	2	US-08-990-114-1
25	36.5	58.9	788	1	US-08-194-338-12
26	36	58.1	313	3	US-08-836-561-106
27	36	58.1	335	1	US-07-947-130-2
28	36	58.1	335	1	US-07-947-130-2

29	36	58.1	335	1	US-08-421-822-2	Sequence 2, Appl1
30	36	58.1	335	1	US-08-421-822-2	Sequence 2, Appl1
31	36	58.1	359	1	US-07-881-075-2	Sequence 2, Appl1
32	36	58.1	359	1	US-08-120-827-2	Sequence 2, Appl1
33	36	58.1	359	1	US-08-478-675-2	Sequence 2, Appl1
34	36	58.1	396	1	US-07-757-390-14	Sequence 14, Appl1
35	36	58.1	396	1	US-08-442-281-14	Sequence 14, Appl1
36	36	58.1	396	1	US-08-442-281-14	Sequence 14, Appl1
37	36	58.1	396	2	US-08-939-727-14	Sequence 14, Appl1
38	36	58.1	420	1	US-07-757-390-13	Sequence 13, Appl1
39	36	58.1	420	1	US-08-442-281-13	Sequence 13, Appl1
40	36	58.1	420	2	US-08-442-281-13	Sequence 13, Appl1
41	36	58.1	420	2	US-08-939-727-13	Sequence 6, Appl1
42	36	58.1	453	1	US-07-956-700B-6	Sequence 6, Appl1
43	36	58.1	453	1	US-08-475-537-6	Sequence 6, Appl1
44	36	58.1	453	1	US-08-485-607-6	Sequence 6, Appl1
45	36	58.1	453	1	US-08-611-107-8	Sequence 8, Appl1

ALIGNMENTS

RESULT 1
US-08-244-951A-4
Sequence 4, Application US/08244951A
Patent No. 5843779
GENERAL INFORMATION:
APPLICANT: VANDERMEEREN, MARC; MERCKEN, MARC;
APPLICANT: VANMECHEREN, EUGEN; VAN DE VOOEDE, ANDRE
TITLE OF INVENTION: MONOCLONAL ANTIBODIES
TITLE OF INVENTION: DIRECTED AGAINST THE MICROTUBULE-ASSOCIATED
TITLE OF INVENTION: PROTEIN TAU, HYBRIDOMAS SECRETING THESE
TITLE OF INVENTION: ANTIBODIES, ANTIGEN RECOGNITION BY THESE
TITLE OF INVENTION: MONOCLONAL ANTIBODIES AND THEIR APPLICATIONS
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESSES:
ADDRESSEE: BIERMAN & MUSERLIAN
STREET: 600 THIRD AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10016
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/244, 951A
FILING DATE: 19-JAN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP93/03499
FILING DATE: 10-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP/92/403403.6
FILING DATE: 14-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: CHARLES A. MUSERLIAN
REGISTRATION NUMBER: 19,683
REFERENCE/DOCKET NUMBER: 410.003A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 661-8000
TELEFAX: (212) 661-8002
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 31
TYPE: Amino Acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
US-08-244-951A-4

Query Match 93.5%; Score 58; DB 2; Length 31;
Best Local Similarity 83.3%; Pred. No. 0.0035;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 KSGSYXPGSPGT 12
DB 4 RSGYSSPGSPGT 15

RESULT 2
US-08-602-264A-10

Sequence 10, Application US/08602264A

Patent No. 5837853

GENERAL INFORMATION:

APPLICANT: AKIHIKO TAKASHIMA et al.

TITLE OF INVENTION: PREVENTIVE OR THERAPEUTIC AGENTS FOR

TITLE OF INVENTION: ALZHEIMER'S DISEASE, A SCREENING METHOD OF ALZHEIMER'S DISEASE

TITLE OF INVENTION: tau-PROTEIN KINASE I ORIGINATED FROM HUMAN BEING (AS AMENDED)

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

ADDRESSEE: WENDROTH, LIND & PONACK

STREET: 805 Fifteenth Street, N.W., #700

CITY: Washington

COUNTRY: D.C.

ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.5 inch,

MEDIUM TYPE: 144 mb

COMPUTER: IBM Compatible

OPERATING SYSTEM: MS-DOS

SOFTWARE: Wordperfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/602,264A

CLASSIFICATION: 514

FILING DATE: February 20, 1996

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/204,091

FILING DATE: March 2, 1994

ATTORNEY/AGENT INFORMATION:

NAME: Warren M. Cheek, Jr.

REGISTRATION NUMBER: 33,367

REFERENCE/DOCKET NUMBER:

TELECOMMUNICATION INFORMATION:

TELEPHONE:

TELEFAX:

TELEX:

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:

LENGTH: 34 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-602-264A-10

Query Match 93.5%; Score 58; DB 2; Length 34;
Best Local Similarity 83.3%; Pred. No. 0.0039;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 KSGSYXPGSPGT 12
DB 4 RSGYSSPGSPGT 15

RESULT 3
US-08-461-018A-10

Sequence 10, Application US/08461018A

Patent No. 6071694

GENERAL INFORMATION:

APPLICANT: AKIHIKO TAKASHIMA et al.

TITLE OF INVENTION: SCREENING METHOD FOR THERAPEUTIC AGENTS AGAINST

TITLE OF INVENTION: ALZHEIMER'S DISEASE (AS AMENDED)

NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: WENDROTH, LIND & PONACK
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
COUNTRY: D.C.
ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.5 inch,

MEDIUM TYPE: 1.44 mb

COMPUTER: IBM Compatible

OPERATING SYSTEM: MS-DOS

SOFTWARE: Wordperfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/461,018A

FILING DATE: June 5, 1995

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/204,091

FILING DATE: March 2, 1994

ATTORNEY/AGENT INFORMATION:

NAME: Warren M. Cheek, Jr.

REGISTRATION NUMBER: 33,367

REFERENCE/DOCKET NUMBER:

TELECOMMUNICATION INFORMATION:

TELEPHONE:

TELEFAX:

TELEX:

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:

LENGTH: 34 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-461-018A-10

Query Match 93.5%; Score 58; DB 3; Length 34;
Best Local Similarity 83.3%; Pred. No. 0.0039;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 KSGSYXPGSPGT 12
DB 4 RSGYSSPGSPGT 15

RESULT 4

US-08-244-951A-1

Sequence 1, Application US/08244951A

Patent No. 5843779

GENERAL INFORMATION:

APPLICANT: VANDERMEEREN, MARC; MERCKEN, MARC;

APPLICANT: VANMECHELEN, EDGEEN; VAN DE VOORDE, ANDRE

TITLE OF INVENTION: MONOCLONAL ANTIBODIES

TITLE OF INVENTION: DIRECTED AGAINST THE MICROTUBULE-ASSOCIATED

TITLE OF INVENTION: PROTEIN TAU, HYBRIDOMAS SECRETING THESE

TITLE OF INVENTION: ANTIBODIES, ANTIGEN RECOGNITION BY THESE

TITLE OF INVENTION: MONOCLONAL ANTIBODIES AND THEIR APPLICATIONS

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:

ADDRESSEE: BIERMAN & MUSERLIAN

STREET: 600 THIRD AVENUE

CITY: NEW YORK

STATE: NEW YORK

COUNTRY: USA

ZIP: 10016

COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY DISK

COMPUTER: IBM PC COMPATIBLE

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: ASCII

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/244,951A
FILING DATE: 19-JAN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP93/03499
FILING DATE: 10-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP/92/403403.6
FILING DATE: 14-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: CHARLES A. MUSERLIAN
REGISTRATION NUMBER: 19,683
REFERENCE/DOCKET NUMBER: 410.003A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 661-8000
TELEFAX: (212) 661-8002
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 67
TYPE: Amino Acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
FEATURE:
NAME/KEY: human tau protein 155-211
US-08-244-951A-1

Query Match 93.5%; Score 58; DB 2; Length 67;
Best Local Similarity 83.3%; Pred. No. 0.0079;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KSGYSXPGSPGT 12
Db 40 RSGYSSPGSPGT 51

RESULT 5
US-08-389-011-1
Sequence 1, Application US/08389011
Patent No. 5861257
GENERAL INFORMATION:
APPLICANT: VANDERMEEREN, MARC; MERCKEN, MARC;
APPLICANT: VANECHELEN, EUGEN; VAN DE VOORDE, ANDRE
TITLE OF INVENTION: MONOCLONAL ANTIBODIES
TITLE OF INVENTION: DIRECTED AGAINST THE MICROTUBULE-ASSOCIATED
TITLE OF INVENTION: PROTEIN TAU, HYBRIDOMAS SECRETING THESE
TITLE OF INVENTION: ANTIBODIES, ANTIGEN RECOGNITION BY THESE
TITLE OF INVENTION: MONOCLONAL ANTIBODIES AND THEIR APPLICATIONS.
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIERMAN & MUSERLIAN
STREET: 600 THIRD AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10016
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/389,011
FILING DATE: 15-FEB-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/403,917
FILING DATE: 19-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/403,916
FILING DATE: 19-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/244,951

FILING DATE: 13-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP93/03499
FILING DATE: 10-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP/92/403403.6
FILING DATE: 14-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: CHARLES A. MUSERLIAN
REGISTRATION NUMBER: 19,683
REFERENCE/DOCKET NUMBER: 410.003-1-CON
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 661-8000
TELEFAX: (212) 661-8002
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 67
TYPE: Amino Acid
STRANDEDNESS: Unknown
TOPOLOGY: Linear
US-08-389-011-1

Query Match 93.5%; Score 58; DB 2; Length 67;
Best Local Similarity 83.3%; Pred. No. 0.0079;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KSGYSXPGSPGT 12
Db 40 RSGYSSPGSPGT 51

RESULT 6
US-08-403-917A-1
Sequence 1, Application US/08403917A
Patent No. 6010913
GENERAL INFORMATION:
APPLICANT: VANDERMEEREN, MARC; MERCKEN, MARC;
APPLICANT: VANECHELEN, EUGEN;
APPLICANT: VAN DE VOORDE, ANDRE
TITLE OF INVENTION: MONOCLONAL ANTIBODIES
TITLE OF INVENTION: DIRECTED AGAINST THE MICROTUBULE-ASSOCIATED
TITLE OF INVENTION: PROTEIN TAU, HYBRIDOMAS SECRETING THESE
TITLE OF INVENTION: ANTIBODIES, ANTIGEN RECOGNITION BY THESE
TITLE OF INVENTION: MONOCLONAL ANTIBODIES AND THEIR APPLICATION
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIERMAN & MUSERLIAN
STREET: 600 THIRD AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10016
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/403,917A
FILING DATE: 19-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/244,951
FILING DATE: 13-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/244,951
FILING DATE: 13-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP93/03499
FILING DATE: 10-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP/92/403403.6
FILING DATE: 14-DEC-1992

ATTORNEY/AGENT INFORMATION:
NAME: CHARLES A. MOSERLIAN
REGISTRATION NUMBER: 19,683
REFERENCE/DOCKET NUMBER: 410,003-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 661-8000
TELEFAX: (212) 661-8002
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 67
TYPE: Amino Acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
US-08-403-917A-1

Query Match 93.5%; Score 58; DB 3; Length 67;
Best Local Similarity 83.3%; Pred. No. 0.0079;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KSGYSPGSPGT 12
DB 40 RSGYSPGSPGT 51

RESULT 7
US-08-776-404B-1
Sequence 1, Application US/08776404B
Patent No. 6121003
GENERAL INFORMATION:
APPLICANT: VANECHELEN, EUGENE
APPLICANT: VAN DE VOORDE, ANDRE
TITLE OF INVENTION: MONOCLONAL ANTIBODIES SPECIFIC FOR AN EPITOPE OF
TITLE OF INVENTION: A PARTICULAR SUBCLASS OR FORM OF PHOSPHORYLATED TAU
TITLE OF INVENTION: HYBRIDOMAS SECRETING THEM, ANTIGEN RECOGNITION OF THESE
TITLE OF INVENTION: ANTIBODIES AND THEIR APPLICATIONS
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: ARNOLD, WHITE & DURKEE
STREET: P.O. BOX 4433
CITY: HOUSTON
STATE: TEXAS
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Microsoft Word 6.0 / ASCII text output
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/776,404B
FILING DATE: 27 Jan 1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP95/03032
FILING DATE: 31 Jul 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 9487031.3
FILING DATE: 29 Jul 1994
ATTORNEY/AGENT INFORMATION:
NAME: KAMMERER, PATRICIA A.
REGISTRATION NUMBER: 29,775
REFERENCE/DOCKET NUMBER: INNS:003
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 106 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-776-404B-1

Query Match 93.5%; Score 58; DB 3; Length 106;

Best Local Similarity 83.3%; Pred. No. 0.013;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 KSGYSPGSPGT 12
DB 49 RSGYSPGSPGT 60

RESULT 8
US-08-666-360-1
Sequence 1, Application US/08666360
Patent No. 6008024
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Monoclonal antibodies specific for PHF-tau,
TITLE OF INVENTION: hybridomas secreting them, antigen recognition of these
TITLE OF INVENTION: antibodies and their applications
NUMBER OF SEQUENCES: 3
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/666,360
FILING DATE:
CLASSIFICATION: 435
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 112 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-666-360-1

Query Match 93.5%; Score 58; DB 3; Length 112;
Best Local Similarity 83.3%; Pred. No. 0.014;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KSGYSPGSPGT 12
DB 52 RSGYSPGSPGT 63

RESULT 9
US-08-159-969-2
Sequence 2, Application US/08159969
Patent No. 5492812
GENERAL INFORMATION:
APPLICANT: VOOHIELS, Paul H.
TITLE OF INVENTION: Diagnostic Method for Alzheimer's
TITLE OF INVENTION: Disease
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/159,969
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/738,778
FILING DATE: 01-AUG-1991

ATTORNEY/AGENT INFORMATION:
NAME: MISTOCK, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 4697-040
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9090
TELEFAX: 212 869-8864/9741
TELEX: 66141 PENNET
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 351 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-159-969-2

Query Match 93.5%; Score 58; DB 1; Length 351;
Best Local Similarity 83.3%; Pred. No. 0.045;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KSGYXPGSPGT 12
:|||||
DB 136 RSGYSSPGSPGT 147

RESULT 10
US-08-726-306A-17
Sequence 17, Application US/08726306A
Patent No. 5958684
GENERAL INFORMATION:
APPLICANT: van Leeuwen, Frederik Willem
APPLICANT: Burbach, Johannes Peter Henri
APPLICANT: Grosveld, Franklin G.
TITLE OF INVENTION: DIAGNOSIS METHOD AND REAGENTS
NUMBER OF SEQUENCES: 189
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Witcoff, Ltd.
STREET: 1 Financial Center
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MB storage
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/726,306A
FILING DATE: 02-Oct-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 95/20080.4
FILING DATE: 02-Oct-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/009,832
FILING DATE: 01-Jan-1996
ATTORNEY/AGENT INFORMATION:
NAME: Williams, Ph.D., Kathleen M.
REGISTRATION NUMBER: 34,380
REFERENCE/DOCKET NUMBER: 96,048-A (3255/00784)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 345-9100
TELEFAX: (617) 345-9111
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 352 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-726-306A-17

Query Match 93.5%; Score 58; DB 2; Length 352;
Best Local Similarity 83.3%; Pred. No. 0.045;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KSGYXPGSPGT 12
:|||||
DB 136 RSGYSSPGSPGT 147

RESULT 11
US-08-244-951A-10
Sequence 10, Application US/08244951A
Patent No. 5843779
GENERAL INFORMATION:
APPLICANT: VANDERMEEREN, MARC; MERCKEN, MARC;
APPLICANT: VANMECHELEN, EUGEN; VAN DE VOEDE, ANDRE
TITLE OF INVENTION: MONOCLONAL ANTIBODIES
TITLE OF INVENTION: DIRECTED AGAINST THE MICROTUBULE-ASSOCIATED
TITLE OF INVENTION: PROTEIN TAU, HYBRIDOMAS SECRETING THESE
TITLE OF INVENTION: ANTIBODIES, ANTIGEN RECOGNITION BY THESE
TITLE OF INVENTION: MONOCLONAL ANTIBODIES AND THEIR APPLICATIONS
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIERMAN & MUSERLIAN
STREET: 600 THIRD AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10016

COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/244,951A
FILING DATE: 19-JAN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP93/03499
FILING DATE: 10-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP/92/403403.6
FILING DATE: 14-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: CHARLES A. MUSERLIAN
REGISTRATION NUMBER: 19,683
REFERENCE/DOCKET NUMBER: 410.003A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 661-8000
TELEFAX: (212) 661-8002
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 391
TYPE: Amino Acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
FEATURE:
NAME/KEY: MTHMPH-tau1 fusion protein
US-08-244-951A-10

Query Match 93.5%; Score 58; DB 2; Length 391;
Best Local Similarity 83.3%; Pred. No. 0.051;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KSGYXPGSPGT 12
:|||||
DB 175 RSGYSSPGSPGT 186

RESULT 12

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US-08-389-011-23
; Sequence 23, Application US/08389011
; Patent No. 5861257
; GENERAL INFORMATION:
; APPLICANT: VANDERMEEREN, MARC; MERCKEN, MARC;
; APPLICANT: VANMECHELEN, EUGEN; VAN DE VOORDE, ANDRE
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES
; TITLE OF INVENTION: DIRECTED AGAINST THE MICROTUBULE-ASSOCIATED
; TITLE OF INVENTION: PROTEIN TAU, HYBRIDOMAS SECRETING THESE
; TITLE OF INVENTION: ANTIBODIES, ANTIGEN RECOGNITION BY THESE
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES AND THEIR APPLICATIONS.
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIERMAN & MUSERLIAN
; STREET: 600 THIRD AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10016
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/389,011
; FILING DATE: 15-FEB-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/403,917
; FILING DATE: 19-JAN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/403,916
; FILING DATE: 19-JAN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/244,951
; FILING DATE: 13-JUN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP93/03499
; FILING DATE: 10-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP/92/403403.6
; FILING DATE: 14-DEC-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: CHARLES A. MUSERLIAN
; REGISTRATION NUMBER: 19,683
; REFERENCE/DOCKET NUMBER: 410.003-1-CON
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 661-8000
; TELEFAX: (212) 661-8002
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 391
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; US-08-389-011-23

Query Match          93.5%; Score 58; DB 2; Length 391;
Best Local Similarity 83.3%; Pred. No. 0.051;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 KSGYXPGSPGT 12
;|||||
Db      175 RSGYSSPGSPGT 186

RESULT 13
; Sequence 23, Application US/08403917A
; Patent No. 6010913
; GENERAL INFORMATION:

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; APPLICANT: VANDERMEEREN, MARC; MERCKEN, MARC;
; APPLICANT: VANMECHELEN, EUGEN;
; APPLICANT: VAN DE VOORDE, ANDRE
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES
; TITLE OF INVENTION: DIRECTED AGAINST THE MICROTUBULE-ASSOCIATED
; TITLE OF INVENTION: PROTEIN TAU, HYBRIDOMAS SECRETING THESE
; TITLE OF INVENTION: ANTIBODIES, ANTIGEN RECOGNITION BY THESE
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES AND THEIR APPLICATION
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIERMAN & MUSERLIAN
; STREET: 600 THIRD AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10016
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/403,917A
; FILING DATE: 19-JAN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/256,167
; FILING DATE: 27-JUN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/244,951
; FILING DATE: 13-JUN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP93/03499
; FILING DATE: 10-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP/92/403403.6
; FILING DATE: 14-DEC-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: CHARLES A. MUSERLIAN
; REGISTRATION NUMBER: 19,683
; REFERENCE/DOCKET NUMBER: 410.003-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 661-8000
; TELEFAX: (212) 661-8002
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 391
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; US-08-403-917A-23

Query Match          93.5%; Score 58; DB 3; Length 391;
Best Local Similarity 83.3%; Pred. No. 0.051;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 KSGYXPGSPGT 12
;|||||
Db      175 RSGYSSPGSPGT 186

RESULT 14
; Sequence 5, Application US/08244951A
; Patent No. 5843779
; GENERAL INFORMATION:
; APPLICANT: VANDERMEEREN, MARC; MERCKEN, MARC;
; APPLICANT: VANMECHELEN, EUGEN; VAN DE VOORDE, ANDRE
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES
; TITLE OF INVENTION: DIRECTED AGAINST THE MICROTUBULE-ASSOCIATED
; TITLE OF INVENTION: PROTEIN TAU, HYBRIDOMAS SECRETING THESE
; TITLE OF INVENTION: ANTIBODIES, ANTIGEN RECOGNITION BY THESE
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES AND THEIR APPLICATIONS

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;
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIERMAN & MUSSELLIAN
; STREET: 600 THIRD AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10016
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/244,951A
; FILING DATE: 19-JAN-1995
; CLASSIFICATION: 435
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP93/03499
; FILING DATE: 10-DEC-1993
;
; APPLICATION NUMBER: EP/92/403403.6
; FILING DATE: 14-DEC-1992
;
; ATTORNEY/AGENT INFORMATION:
; NAME: CHARLES A. MUSSELLIAN
; REGISTRATION NUMBER: 19,683
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 661-8000
; TELEFAX: (212) 661-8002
;
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
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; US-08-244-951A-5
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; Query Match 90.3%; Score 56; DB 2; Length 27;
; Best Local Similarity 90.3%; Pred. No. 0.0062;
; Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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; QY 2 SGXSXPGSPGT 12
; DB 3 SGXSXPGSPGT 13
;
;
; RESULT 15
; US-08-411-777-8
; Sequence 8, Application US/08411777
; Patent No. 5792641
;
; GENERAL INFORMATION:
; APPLICANT: Schuelein, Martin
; APPLICANT: Fredholm, Henrik
; APPLICANT: Hjorth, Carsten
; APPLICANT: Rasmussen, Grethe
; APPLICANT: Nielsen, Egon
; APPLICANT: Rosholm, Peter
; TITLE OF INVENTION: Cellulase Variants
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5792641 of No. 5792641 of America
; STREET: 405 Lexington Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10174-6401
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0

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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/411,777
; FILING DATE: 05-MAY-1995
; CLASSIFICATION: 435
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Gregg, Valeria A
; REGISTRATION NUMBER: 35,127
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-868-9655
;
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 252 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 5792641e
;
; US-08-411-777-8
;
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; Query Match 62.9%; Score 39; DB 1; Length 252;
; Best Local Similarity 54.5%; Pred. No. 31;
; Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
;
; QY 2 SGXSXPGSPGT 12
; DB 99 SSYNAPGDPGS 109
;

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Search completed: October 2, 2000, 18:03:51
Job time: 1876 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: October 2, 2000, 18:02:13 ; Search time 84.99 Seconds
(without alignments)
4.375 Million cell updates/sec

Title: US-09-142-613-2

Perfect score: 62
Sequence: 1 KSGYKXPGSPGT 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 85661 seqs, 30989116 residues

Total number of hits satisfying chosen parameters: 85661

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database: SwissProt_38.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	58	93.5	341	1	TAU3_MOUSE
2	58	93.5	341	1	TAU2_MOUSE
3	58	93.5	402	1	TAU3_BOVIN
4	58	93.5	432	1	TAU_RAT
5	58	93.5	441	1	TAU_HUMAN
6	58	93.5	448	1	TAU1_BOVIN
7	42	67.7	1986	1	WA_EMENT
8	41	66.1	640	1	SYVM_PODAN
9	41	66.1	963	1	YQ36_CAEEL
10	40	64.5	680	1	CA1A_MOUSE
11	40	64.5	766	1	PIPB_HUMAN
12	40	64.5	1387	1	RGSC_RAT
13	40	64.5	1758	1	CA14_CAEEL
14	40	64.5	1758	1	CA24_CAEEL
15	39	62.9	447	1	ACCC_ANASP
16	39	62.9	511	1	GUNB_PSEFL
17	39	62.9	828	1	MRKC_KLEPN
18	38	61.3	680	1	CA1A_HUMAN
19	38	61.3	870	1	YQ35_CAEEL
20	37	59.7	449	1	GAD_MOUSE
21	37	59.7	449	1	GAD_RAT
22	37	59.7	635	1	CA28_HUMAN
23	37	59.7	1763	1	CA24_JASCU
24	37	59.7	1827	1	MAP2_HUMAN
25	37	59.7	1828	1	MAP2_MOUSE
26	37	59.7	1861	1	MAP2_RAT
27	36	58.1	310	1	RCEL_CHLAU
28	36	58.1	415	1	VE2_PAPYE
29	36	58.1	418	1	NTR1_HUMAN
30	36	58.1	420	1	ILSR_HUMAN
31	36	58.1	782	1	FLIR_RAT
32	36	58.1	976	1	MGR_DROME
33	36	58.1	1876	1	GLS1_YEAST

34	35.5	57.3	467	1	RPB1_CRIGR
35	35.5	57.3	1970	1	RPB1_HUMAN
36	35.5	57.3	1970	1	RPB1_MOUSE
37	35	56.5	209	1	COEC_SCYCA
38	35	56.5	251	1	C10B_HUMAN
39	35	56.5	316	1	CC12_CAEEL
40	35	56.5	316	1	CC13_CAEEL
41	35	56.5	317	1	VB05_VACCO
42	35	56.5	317	1	VB05_VACCV
43	35	56.5	317	1	VB05_VACCV
44	35	56.5	351	1	OPSP_CHICK
45	35	56.5	415	1	ILSR_MOUSE

ALIGNMENTS

RESULT 1
ID TAU3_MOUSE STANDARD; PRT; 341 AA.
AC P10637;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE MICROTUBULE-ASSOCIATED PROTEIN TAU (CLONE TAU).
GN MAPT OR MAPT.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN (1)
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN;
RX MEDLINE: 88099510.
RT Lee G., Cowan N.J., Kirschner M.;
RT "The primary structure and heterogeneity of tau protein from mouse brain."
RL Science 239:285-288(1988).
CC -1- FUNCTION: TAU PROTEIN PROMOTES MICROTUBULE ASSEMBLY AND STABILIZES MICROTUBULES.
CC -1- ALTERNATIVE PRODUCTS: THE DIFFERENT FORMS OF TAU SEEM TO BE PRODUCED BY ALTERNATIVE SPLICING.
CC -1- DOMAIN: THE REPEATED DOMAIN BINDS TO TUBULIN.
CC -1- PTM: VARIOUS SERINE RESIDUES IN THE REPEATS MAY BE PHOSPHORYLATED BY CAMP KINASE.
CC -1- SIMILARITY: CONTAINS 3 TAU/MAP REPEATS.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb.slb.ch/announce/> or send an email to license@isb.slb.ch).
CC -----
DR EMBL: M18775; AAA04165.1; -
DR PIR: B28820; B28820.
DR MGD: MGT:97180; MTAPT.
DR PFAM: PF00418; tubulin-binding; 3.
DR PROSITE: PS00229; TAU_MAP_1; 3.
KW Microtubules; Repeat; Alternative splicing.
FT REPEAT 175 205 TAU/MAP MOTIF.
FT REPEAT 206 236 TAU/MAP MOTIF.
FT REPEAT 237 268 TAU/MAP MOTIF.
SQ SEQUENCE 341 AA; 35714 MW; 476641931A5A143 CRC64;

Query Match 93.5%; Score 58; DB 1; Length 341;

Best Local Similarity 83.3%; Pred. No. 0.015; Mismatches 1; Indels 0; Gaps 0;

Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KSGYKXPGSPGT 12
DB 125 RSGYKXPGSPGT 136

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RESULT 2
TAU2_MOUSE STANDARD; PRT; 364 AA.
ID TAU2_MOUSE
AC P10638;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE MICROTUBULE-ASSOCIATED PROTEIN TAU (CLONE TAU2).
GN MAPT OR MTAPT.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN;
RX MEDLINE; 88099510.
RA Lee G., Cowan N.J., Kirschner M.;
RT "The primary structure and heterogeneity of tau protein from mouse
RT brain."
RL Science 239:285-288(1988).
CC -1- FUNCTION: TAU PROTEIN PROMOTES MICROTUBULE ASSEMBLY AND STABILIZES
CC MICROTUBULES.
CC -1- ALTERNATIVE PRODUCTS: THE DIFFERENT FORMS OF TAU SEEM TO BE
CC PRODUCED BY ALTERNATIVE SPLICING.
CC -1- DOMAIN: THE REPEATED DOMAIN BINDS TO TUBULIN.
CC -1- PTM: VARIOUS SERINE RESIDUES IN THE REPEATS MAY BE PHOSPHORYLATED
CC BY CAMP KINASE.
CC -1- SIMILARITY: CONTAINS 3 TAU/MAP REPEATS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M18776; AAA40166.1; -
DR PIR; A28820; A28820.
DR MGD; MGI:97180; MTAPT.
DR PFAM; PF00418; tubulin-binding; 3.
DR PROSITE; PS00229; TAU_MAP_1; 3.
KM Microtubules; Repeat; Alternative splicing.
FT REPEAT 175 205 TAU/MAP MOTIF.
FT REPEAT 206 236 TAU/MAP MOTIF.
FT REPEAT 237 268 TAU/MAP MOTIF.
SQ SEQUENCE 364 AA; 38199 MW; DICAB2EF89CDD7C0 CRC64;

Query Match 93.5%; Score 58; DB 1; Length 364;
Best Local Similarity 83.3%; Pred. No. 0.016;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KSGYSPGSPGT 12
Db 125 RSGYSPGSPGT 136

```

```

RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 89261765.
RA Himmler A., Drechsel D., Kirschner M.W., Martin D.W. Jr.;
RT "Tau consists of a set of proteins with repeated C-terminal
RT microtubule-binding domains and variable N-terminal domains."
RL Mol. Cell. Biol. 9:1381-1388(1989).
CC -1- FUNCTION: TAU PROTEIN PROMOTES MICROTUBULE ASSEMBLY AND STABILIZES
CC MICROTUBULES.
CC -1- ALTERNATIVE PRODUCTS: THE DIFFERENT FORMS OF TAU SEEM TO BE
CC PRODUCED BY ALTERNATIVE SPLICING.
CC -1- DOMAIN: THE REPEATED DOMAIN BINDS TO TUBULIN.
CC -1- PTM: VARIOUS SERINE RESIDUES IN THE REPEATS MAY BE PHOSPHORYLATED
CC BY CAMP KINASE.
CC -1- SIMILARITY: CONTAINS 3 OR 4 TAU/MAP REPEATS.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M26158; AAA30771.1; -
DR PIR; B31939; ORB02.
DR PFAM; PF00418; tubulin-binding; 4.
DR PROSITE; PS00229; TAU_MAP_1; 4.
KM Microtubules; Repeat; Alternative splicing.
FT REPEAT 205 235 TAU/MAP MOTIF.
FT REPEAT 236 266 TAU/MAP MOTIF.
FT REPEAT 267 297 TAU/MAP MOTIF.
FT REPEAT 298 329 TAU/MAP MOTIF.
FT VARSPIC 1 100 MISSING (IN ISOBORN 4).
FT VARSPIC 235 295 MISSING (IN ISOBORN 5).
SQ SEQUENCE 402 AA; 42232 MW; A7FCE47A0AD7340 CRC64;

Query Match 93.5%; Score 58; DB 1; Length 402;
Best Local Similarity 83.3%; Pred. No. 0.016;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KSGYSPGSPGT 12
Db 155 RSGYSPGSPGT 166

RESULT 4
TAU_RAT STANDARD; PRT; 432 AA.
ID TAU_RAT
AC P19332;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE MICROTUBULE-ASSOCIATED PROTEIN TAU.
GN MAPT OR MTAPT.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN;
RX MEDLINE; 90180457.
RA Kosik K.S., Orecchio L.D., Bakalis S., Neve R.L.;
RT "Developmentally regulated expression of specific tau sequences."
RL Neuron 2:1389-1397(1989).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE; 89359509.
RA Kanai Y., Takemura R., Oshima T., Mori H., Ihara Y., Yanagisawa M.,
RA Masaki T., Hirokawa N.;
RT "Expression of multiple tau isoforms and microtubule bundle formation
RT in fibroblasts transfected with a single tau cDNA."

```

RL J. Cell Biol. 109:1173-1184(1989).
 CC -1- FUNCTION: TAU PROTEIN PROMOTES MICROTUBULE ASSEMBLY AND STABILIZES
 CC MICROTUBULES.
 CC -1- ALTERNATIVE PRODUCTS: THE DIFFERENT FORMS OF TAU SEEM TO BE
 CC PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- DOMAIN: THE REPEATED DOMAIN BINDS TO TUBULIN.
 CC -1- PTM: VARIOUS SERINE RESIDUES IN THE REPEATS MAY BE PHOSPHORYLATED
 CC BY CAMP KINASE.
 CC -1- SIMILARITY: CONTAINS 3 OR 4 TAU/MAP REPEATS.
 DR PIR: J03036; J03036.
 DR PIR: A33574; A33574.
 DR PFAM: PF00418; tubulin-binding; 4.
 DR PROSITE: PS00229; TAU_MAP.1; 4.
 KM Microtubules; Repeat: Alternative splicing: Phosphorylation.
 FT REPEAT 235 265 TAU/MAP MOTIF.
 FT REPEAT 266 296 TAU/MAP MOTIF.
 FT REPEAT 297 327 TAU/MAP MOTIF.
 FT REPEAT 328 359 TAU/MAP MOTIF.
 FT DISULFID 282 313 BY SIMILARITY.
 FT MOD_RES 347 347 PHOSPHORYLATION (BY CAMP) (POTENTIAL).
 FT VARSPPLIC 266 296 MISSING (IN FETAL ISOFORM).
 SO SEQUENCE 432 AA; 45113 MW; A4810DF6CF04457F CRC64;

Query Match 93.5%; Score 58; DB 1; Length 432;
 Best Local Similarity 83.3%; Pred. No. 0.019;
 Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KSGYSXPGSPGT 12
 :|||||
 DB 185 RSGYSSPGSPGT 196

RESULT 5
 TAU_HUMAN STANDARD; PRT; 441 AA.
 ID TAU_HUMAN
 AC TAU0636; P18518; Q14799; Q15551;
 DT 01-JUL-1989 (Rel. 11, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE MICROTUBULE-ASSOCIATED PROTEIN TAU.
 GN MAPT OR MTBR1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 RN
 RP SEQUENCE FROM N.A.
 RA MEDLINE; 93041757.
 RX Andreadis A., Brown W.M., Kosik K.S.;
 RT "Structure and novel exons of the human tau gene.";
 RL Biochemistry 31:10626-10633(1992).
 RN
 RP SEQUENCE OF 1-44 AND 103-441 FROM N.A.
 RC TISSUE-BRAIN;
 RX MEDLINE; 89251564.
 RA Goedert M., Spillantini M.G., Potter M.C., Ulrich J., Crowther R.A.;
 RT "Cloning and sequencing of the cDNA encoding an isoform of
 RT microtubule-associated protein tau containing four tandem repeats:
 RT differential expression of tau protein mRNAs in human brain.";
 RL EMBO J. 8:393-399(1989).
 RN
 RP SEQUENCE OF 1-26 AND 306-441 FROM N.A.
 RC TISSUE-BRAIN;
 RX MEDLINE; 88234557.
 RA Goedert M., Wischik C., Crowther R., Walker J., Klug A.;
 RT "Cloning and sequencing of the cDNA encoding a core protein of the
 RT paired helical filament of Alzheimer disease: identification as the
 RT microtubule-associated protein tau.";
 RL Proc. Natl. Acad. Sci. U.S.A. 85:4051-4055(1988).
 RN
 RP SEQUENCE OF 1-26 AND 306-441 FROM N.A.
 RC TISSUE-BRAIN;
 RX MEDLINE; 90180482.

RA Lee G., Neve R.L., Kosik K.S.;
 RT "The microtubule binding domain of tau protein.";
 RL Neuron 2:1615-1624(1989).
 CC -1- FUNCTION: TAU PROTEIN PROMOTES MICROTUBULE ASSEMBLY AND STABILIZES
 CC MICROTUBULES.
 CC -1- ALTERNATIVE PRODUCTS: THE DIFFERENT FORMS OF TAU SEEM TO BE
 CC PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- DOMAIN: THE REPEATED DOMAIN BINDS TO TUBULIN.
 CC -1- PTM: VARIOUS SERINE RESIDUES IN THE REPEATS MAY BE PHOSPHORYLATED
 CC BY CAMP KINASE.
 CC -1- DISEASE: TAU CONSTITUTES AT LEAST A PART OF THE PAIRED HELICAL
 CC FILAMENT (PHF) CORE IN ALZHEIMER DISEASE.
 CC -1- SIMILARITY: CONTAINS 3 OR 4 TAU/MAP REPEATS.
 CC -1- DATABASE: NAME=HOMOCLECHASE; NOTE=tau entry;
 CC WWW="http://biolinformatics.welzmann.ac.at/hotmolechase/entries/tau.htm".
 CC -----
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 CC -----

DR EMBL: AF027491; AAC04279.1; -
 DR EMBL: AF047856; AAC04279.1; JOINED.
 DR EMBL: AF047857; AAC04279.1; JOINED.
 DR EMBL: AF027492; AAC04279.1; JOINED.
 DR EMBL: AF027493; AAC04279.1; JOINED.
 DR EMBL: AF047860; AAC04279.1; JOINED.
 DR EMBL: AF047862; AAC04279.1; JOINED.
 DR EMBL: AF027494; AAC04279.1; JOINED.
 DR EMBL: AF027495; AAC04279.1; JOINED.
 DR EMBL: AF027496; AAC04279.1; JOINED.
 DR EMBL: AF047863; AAC04279.1; JOINED.
 DR EMBL: AF027491; AAC04278.1; -
 DR EMBL: AF027492; AAC04278.1; JOINED.
 DR EMBL: AF027493; AAC04278.1; JOINED.
 DR EMBL: AF047860; AAC04278.1; JOINED.
 DR EMBL: AF047862; AAC04278.1; JOINED.
 DR EMBL: AF027495; AAC04278.1; JOINED.
 DR EMBL: AF027496; AAC04278.1; JOINED.
 DR EMBL: AF047863; AAC04278.1; JOINED.
 DR EMBL: J03778; AAA60615.1; -
 DR EMBL: X14474; CAA32636.1; -
 DR PIR: A30217; QRHTU1.
 DR PIR: P00001; QRHTU2.
 DR PIR: S03796; S03796.
 DR MIM: 157140; -
 DR PFAM: PF00418; tubulin-binding; 4.
 DR PROSITE: PS00229; TAU_MAP.1; 4.
 KM Microtubules; Repeat: Alternative splicing: Phosphorylation.
 FT REPEAT 244 274 TAU/MAP MOTIF.
 FT REPEAT 275 305 TAU/MAP MOTIF.
 FT REPEAT 306 336 TAU/MAP MOTIF.
 FT REPEAT 337 368 TAU/MAP MOTIF.
 FT DISULFID 291 332 BY SIMILARITY.
 FT VARSPPLIC 45 102 MISSING (IN ISOFORM 1 AND ISOFORM 3).
 FT VARSPPLIC 275 305 MISSING (IN ISOFORM 2 AND ISOFORM 3).
 FT VARSPPLIC 1 44 MAEPREFEVEDHAGTIGLGRKQGGITTHQDEGDTDA
 FT FT GLK -> MIRAQQQRK (IN FETAL ISOFORM).
 SO SEQUENCE 441 AA; 45850 MW; 835A8706D847A8CC CRC64;

Query Match 93.5%; Score 58; DB 1; Length 441;
 Best Local Similarity 83.3%; Pred. No. 0.019;
 Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KSGYSXPGSPGT 12
 :|||||
 DB 194 RSGYSSPGSPGT 205

RESULT 6
TAU1_BOVIN STANDARD; PRT: 448 AA.
ID TAU1_BOVIN STANDARD; PRT: 448 AA.
AC P29172;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE MICROTUBULE-ASSOCIATED PROTEIN TAU FORMS 1 AND 2.
GN MAPT.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 89261765.
RA Hammler A., Drechsel D., Kirschner M.W., Martin D.W. Jr.;
RT "Tau consists of a set of proteins with repeated C-terminal
microtubule-binding domains and variable N-terminal domains";
RL Mol. Cell. Biol. 9:1381-1388(1989).
CC -1- FUNCTION: TAU PROTEIN PROMOTES MICROTUBULE ASSEMBLY AND STABILIZES
MICROTUBULES.
CC -1- ALTERNATIVE PRODUCTS: THE DIFFERENT FORMS OF TAU SEEM TO BE
PRODUCED BY ALTERNATIVE SPLICING.
CC -1- DOMAIN: THE REPEATED DOMAIN BINDS TO TUBULIN.
CC -1- PTM: VARIOUS SERINE RESIDUES IN THE REPEATS MAY BE PHOSPHORYLATED
BY CAMP KINASE.
CC -1- SIMILARITY: CONTAINS 4 TAU/MAP REPEATS.
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CC EMBL: L34953; AAA51609.1; -
DR EMBL: L34940; AAA51609.1; JOINED.
DR EMBL: L34941; AAA51609.1; JOINED.
DR EMBL: L34942; AAA51609.1; JOINED.
DR EMBL: L34943; AAA51609.1; JOINED.
DR EMBL: L34944; AAA51609.1; JOINED.
DR EMBL: L34945; AAA51609.1; JOINED.
DR EMBL: L34946; AAA51609.1; JOINED.
DR EMBL: L34947; AAA51609.1; JOINED.
DR EMBL: L34948; AAA51609.1; JOINED.
DR EMBL: L34949; AAA51609.1; JOINED.
DR EMBL: L34950; AAA51609.1; JOINED.
DR EMBL: L34951; AAA51609.1; JOINED.
DR EMBL: L34952; AAA51609.1; JOINED.
DR EMBL: M26157; AAA30770.1; -
DR PIR: A31939; ORBOT1.
DR PFAM: PF00418; tubulin-binding; 4.
DR PROSITE: PS00229; TAU/MAP.1; 4.
KW Microtubules; Repeat; Alternative splicing.
FT REPEAT 251 281 TAU/MAP MOTIF.
FT REPEAT 282 312 TAU/MAP MOTIF.
FT REPEAT 313 343 TAU/MAP MOTIF.
FT REPEAT 344 375 TAU/MAP MOTIF.
FT VARSPLIC 175 192 MISSING (IN ISOFORM 2).
SQ SEQUENCE 448 AA; 46332 MW; 821638A8C4809602 CRC64;

Query Match 93.5%; Score 58; DB 1; Length 448;
Best Local Similarity 83.3%; Pred. No. 0.02;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KSGTSPGSPGT 12
DB 201 KSGTSPGSPGT 212

RESULT 7
WA_EMENTI STANDARD; PRT: 1986 AA.
ID WA_EMENTI STANDARD; PRT: 1986 AA.
AC Q03149;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE CONIDIAL GREEN PIGMENT SYNTHASE (EC 2.3.1.-).
GN WA.
OS Emericella nidulans (Aspergillus nidulans).
OC Eukaryota; Fungi; Ascomycota; Eurotiiales; Trichocomaceae; Emericella.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 93101122.
RA Mayorga M.E., Timberlake W.E.;
RT "The developmentally regulated Aspergillus nidulans wa gene encodes a
polypeptide homologous to polyketide and fatty acid synthases";
RL Mol. Gen. Genet. 235:205-212(1992).
CC -1- FUNCTION: THIS PROTEIN CONDENSES CARBON UNITS TO FORM AN
INTERMEDIATE YELLOW POLYKETIDE PIGMENT THAT IS POLYMERIZED
BY CONIDIAL LACCASE TO FORM THE GREEN PIGMENT IN MATURE
ASEXUAL SPORES (CONIDIA).
CC -1- COFACTOR: CONTAINS 2 COVALENTLY BOUND PHOSPHOPANTETHEINES
(POTENTIAL).
CC -1- PATHWAY: BIOSYNTHESIS OF CONIDIAL GREEN PIGMENT.
CC -1- SIMILARITY: WITH BOTH EUKARYOTIC AND PROKARYOTIC POLYKETIDE
SYNTHASES AND VERTEBRATE FATTY ACID SYNTHASES.
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CC EMBL: X65866; CAA46695.1; -
DR PIR: S28353; S28353.
DR PFAM: PF00668; Acyl-transf. 1.
DR PFAM: PF00109; ketoacyl-synt. 1.
DR PFAM: PF00550; pp-binding; 2.
DR PROSITE: PS00012; PHOSPHOPANTETHEINE; 1.
DR PROSITE: PS00606; B-KETOACYL SYNTHASE; 1.
DR PROSITE: PS50075; ACP DOMAIN; 2.
KW Transferase; Phosphopantetheine; Multifunctional enzyme.
FT DOMAIN 529 562 BETA-KETOACYL SYNTHASE (BY SIMILARITY).
FT DOMAIN 991 1024 ACYL/MALONYL TRANSFERASES
(BY SIMILARITY).
FT DOMAIN 1650 1719 ACYL CARRIER (ACP).
FT DOMAIN 1772 1841 BETA-KETOACYL SYNTHASE (BY SIMILARITY).
FT ACT_SITE 548 548 BETA-KETOACYL SYNTHASE (BY SIMILARITY).
FT ACT_SITE 1001 1001 ACYL/MALONYL TRANSFERASES (BY
SIMILARITY).
FT BINDING 1682 1682 PHOSPHOPANTETHEINE (BY SIMILARITY).
FT BINDING 1804 1804 PHOSPHOPANTETHEINE (BY SIMILARITY).
SQ SEQUENCE 1986 AA; 216634 MW; 74EF0940FF40E5BA CRC64;

Query Match 67.7%; Score 42; DB 1; Length 1986;
Best Local Similarity 72.7%; Pred. No. 33;
Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 SGTSPGSPGT 12
DB 1746 SGTSPGSPGT 1756
RESULT 8
ID STYM_PODAN STANDARD; PRT: 640 AA.
AC P28669;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)

DT 01-OCT-1996 (rel. 34, Last annotation update)
 DE TYROSYL-TRNA SYNTHETASE, MITOCHONDRIAL PRECURSOR (EC 6.1.1.1)
 DE (TYROSINE--TRNA LIGASE) (TYRS).
 GN YTS1.
 OS Podospora anserina.
 OC Eukaryota; Fungi; Ascomycota; Sordariales; Sordariaceae; Podospora.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-S-;
 RX MEDLINE: 92123176.
 RA Kaempfer U., Knecht U., Cherniak A.D., Lambowitz A.M.;
 RT "The mitochondrial tyrosyl-TRNA synthetase of Podospora anserina is a
 RT bifunctional enzyme active in protein synthesis and RNA splicing.";
 RT Mol. Cell. Biol. 12:499-511(1992).
 RL
 CC -1- FUNCTION: HAS BOTH A AMINOACYL-TRNA SYNTHETASE ACTIVITY AND IS
 CC INVOLVED IN THE SPLICING OF GROUP 1 INTRONS.
 CC -1- CATALYTIC ACTIVITY: ATP + L-TYROSINE + TNA(UTR) = AMP +
 CC PYROPHOSPHATE + L-TYROSYL-TRNA(UTR).
 CC -1- SUBCELLULAR LOCATION: MITOCHONDRIAL MATRIX.
 CC -1- SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.
 CC
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 CC
 CC EMBL: Y54981; CAA38725.1; -
 CC PIR: S38781; S38781.
 DR HSSP: P00952; ITVA.
 DR PFAM: P00579; tRNA-syn-1b; 1.
 DR PRINTS: PR01040; TRNASYNTHTR.
 DR PROSITE: PS00178; AA-TRNA-LIGASE-1; 1.
 DR Aminoacyl-TRNA synthetase: Protein biosynthesis; Ligase; ATP-binding;
 KM Mitochondrion; Transl. peptide; mRNA processing.
 FT TRANSIT 1
 FT CHAIN 7
 FT SIMILAR 105 114 TYROSYL-TRNA SYNTHETASE.
 FT SIMILAR 322 326 "HIGH" REGION.
 FT BINDING 325 325 "KMSKS" REGION.
 FT BINDING 325 325 ATP (BY SIMILARITY).
 SQ SEQUENCE 640 AA; 72406 MW; 1DBA1C469FF5E5C6 CRC64;
 Query Match
 Best Local Similarity 66.1%; Score 41; DB 1; Length 640;
 Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 QY 1 KSGYKPGSPGT 12
 DB 551 ESGQTYPERGT 562
 RESULT 9
 ID Y036_CAEEL STANDARD; PRI: 963 AA.
 AC 009457;
 DT 01-NOV-1997 (rel. 35, Created)
 DT 01-NOV-1997 (rel. 35, Last sequence update)
 DT 01-NOV-1997 (rel. 35, Last annotation update)
 DE PUTATIVE CUTICLE COLLAGEN C0965.6.
 GN C0965.6.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RA Palmer S.;
 RL Submitted (NOV-1994) to the EMBL/GenBank/DBS databases.
 CC -1- FUNCTION: NEMATODE CUTICLES ARE COMPOSED LARGELY OF COLLAGEN-LIKE
 CC PROTEINS. THE CUTICLE FUNCTIONS BOTH AS AN EXOSKELETON AND AS A

CC BARRIER TO PROTECT THE WORM FROM ITS ENVIRONMENT (BY SIMILARITY).
 CC -1- SUBUNIT: COLLAGEN POLYPEPTIDE CHAINS ARE COMPLEXED WITHIN THE
 CC CUTICLE BY DISULFIDE BONDS AND OTHER TYPES OF COVALENT CROSS-
 CC LINKS (BY SIMILARITY).
 CC -1- SIMILARITY: TO OTHER COLLAGENS. STRONG, TO OTHER CUTICLE
 CC COLLAGENS.
 CC
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 CC
 CC EMBL: 246791; CAA6755.1; -
 CC WORMPEP: C0965.6; CE01486.
 DR PFAM: PF01484; COLCUTICLE_N; 1.
 DR PFAM: PF01391; Collagen; 2.
 DR Hypothetical protein; Cuticle; Connective tissue; Repeat;
 KM Multigene family; Collagen.
 FT DOMAIN 392 423 TRIPLE-HELICAL REGION.
 FT DOMAIN 441 503 TRIPLE-HELICAL REGION.
 FT DOMAIN 506 567 TRIPLE-HELICAL REGION.
 FT DOMAIN 663 666 POLY-PRO.
 FT DOMAIN 685 688 POLY-PRO.
 SQ SEQUENCE 963 AA; 107031 MW; AFF895A75909F66E CRC64;
 Query Match
 Best Local Similarity 66.1%; Score 41; DB 1; Length 963;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 3 GYSKPGSPGT 12
 DB 557 GVSAPGAPGT 566
 RESULT 10
 ID CALA_MOUSE STANDARD; PRI: 680 AA.
 AC 005306;
 DT 01-NOV-1995 (rel. 32, Last sequence update)
 DT 01-NOV-1995 (rel. 32, Last annotation update)
 DE COLLAGEN ALPHA 1(X) CHAIN PRECURSOR.
 GN COL10A1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BALB/C;
 RX MEDLINE: 93143676.
 RA Elima K., Berola I., Rosati R., Metsaranta M., Garofalo S., Perala M.,
 RA de Crombrughe B., Vuorio E.;
 RT "The mouse collagen X gene: complete nucleotide sequence, exon
 RT structure and expression pattern.";
 RL Biochem. J. 289:247-253(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-129/SV; TISSUE-LIVER;
 RX MEDLINE: 93238750.
 RA Kong R.Y.C., Kwan K.M., Lau E.T., Thomas J.T., Boot-Handford R.P.,
 RA Grant M.E., Cheah K.S.E.;
 RT "Intron-exon structure, alternative use of promoter and expression of
 RT the mouse collagen X gene, Col10a-1.";
 RL Eur. J. Biochem. 213:39-111(1993).
 RN [3]
 RP SEQUENCE OF 51-680 FROM N.A.
 RC STRAIN-DBA/2J;
 RX MEDLINE: 92267014.
 RA Apte S.S., Seidlin M.F., Hayashi M., Olsen B.R.;

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RT "Cloning of the human and mouse type X collagen genes and mapping of
RT the mouse type X collagen gene to chromosome 10."
RL Eur. J. Biochem. 206:217-224(1992).
RN [4]
RP SEQUENCE OF 385-627 FROM N.A.
RC STRAIN-C57BL.
RX MEDLINE: 92182017.
RA Elima K., Metsaeranta M., Kallio J., Peraeae M., Eroola I.,
RA Garofalo S., de Crombrughe B., Vuorio E.;
RT "Specific hybridization probes for mouse alpha 2(I)X and alpha 1(X)
RT collagen mRNAs."
RL Biochim. Biophys. Acta 1130:78-80(1992).
CC -1- FUNCTION: TYPE X COLLAGEN IS A PRODUCT OF HYPERTROPHIC
CC CHONDROCYTES AND HAS BEEN LOCALIZED TO PRESUMPTIVE
CC MINERALIZATION ZONES OF HYALINE CARTILAGE.
CC -1- SUBUNIT: HOMOTRIMER.
CC -1- UNIT: PROLINES AT THE THIRD POSITION OF THE TRIPEPTIDE REPEATING
CC UNIT (G-X-Y) ARE HYDROXYLATED IN SOME OR ALL OF THE CHAINS.
CC -1- SIMILARITY: STRONG, TO ALPHA 1 AND 2 TYPE VIII COLLAGENS.
CC -1- SIMILARITY: CONTAINS 1 C10 DOMAIN.
CC -----
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CC -----
DR EMBL: X67348: CAA47763.1: -
DR EMBL: X65121: CAA46237.1: -
DR EMBL: X63013: CAA44741.1: -
DR EMBL: Z21610: CAA79736.1: -
DR PIR: S28807: S28807.
DR PIR: S31216: S31216.
DR MGD: MGI:88445: COL10A1.
DR PIR: P000386: C1Q: 1.
DR PIR: P01381: Collagen: 6.
DR PRINTS: P00007: COMPLEMENTC1Q.
DR PROSITE: PS01133: C1Q: 1.
KM Extracellular matrix; Connective tissue; Repeat; Hydroxylation;
KM Cartilage; Collagen; Signal.
FT SIGNAL 1 18
FT CHAIN 19 680
FT DOMAIN 19 56
FT DOMAIN 57 519
FT DOMAIN 520 680
FT DOMAIN 545 680
FT CONFLICT 248 248
FT CONFLICT 286 286
FT CONFLICT 306 306
FT CONFLICT 417 417
FT CONFLICT 451 451
FT CONFLICT 500 500
FT CONFLICT 567 567
FT CONFLICT 569 569
FT CONFLICT 571 572
FT CONFLICT 635 635
SO SEQUENCE 680 AA: 66775 MW: FE984CA9A9AF708E2 CRC64;

Query Match 64.5%; Score 40; DB 1; Length 680;
Best Local Similarity 54.5%; Pred. No. 24;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

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ID PIP6_HUMAN STANDARD; PRT; 756 AA.
AC P51178;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-FEB-2000 (Rel. 39, Last annotation update)
DE 1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHOLIPASE DELTA 1
DE (EC 3.1.4.11) (PLC-DELTA-1) (PHOSPHOLIPASE C-DELTA-1) (PLC-III).
GN PLCD1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-NORTH;
RX MEDLINE: 95197554.
RA Cheng H.F., Jiang M.J., Chen C.L., Liu S.M., Wong L.P.,
RA Lomasney J.W., King K.;
RT "Cloning and identification of amino acid residues of human
RT phospholipase C delta 1 essential for catalysis."
RL J. Biol. Chem. 270:5495-5505(1995).
CC -1- FUNCTION: THE PRODUCTION OF THE SECOND MESSENGER MOLECULES
CC DIACYLGLYCEROL (DAG) AND INOSITOL 1,4,5-TRISPHOSPHATE (IP3) IS
CC MEDIATED BY ACTIVATED PHOSPHATIDYLINOSITOL-SPECIFIC PHOSPHOLIPASE
CC C ENZYMES.
CC -1- CATALYTIC ACTIVITY: 1-PHOSPHATIDYL-D-MYO-INOSITOL 4,5-BISPHOSPHATE
CC + H2O = D-MYO-INOSITOL 1,4,5-TRISPHOSPHATE + DIACYLGLYCEROL.
CC -1- COFACTOR: REQUIRES CALCIUM.
CC -1- MISCELLANEOUS: THERE ARE AT LEAST SIX FORMS OF PLC ENZYMES.
CC -1- SIMILARITY: DOMAINS X AND Y ARE CONSERVED IN DIFFERENT FORMS OF
CC PLC AND ARE ESSENTIAL FOR CATALYTIC ACTIVITY.
CC -1- SIMILARITY: CONTAINS 1 C2 DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 PH DOMAIN.
CC -1- SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING DOMAINS.
CC -----
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CC -----
DR EMBL: U09117: AAA73567.1: -
DR HSSP: P10688; IMAT.
DR KIM: 602142; -
DR PIR: P00168: C2: 1.
DR PIR: P00169: PH: 1.
DR PIR: P00388: PI-PLC-X: 1.
DR PIR: P00387: PI-PLC-Y: 1.
DR PIR: P00036: ehand: 1.
DR PRINTS: P00360: C2DOMAIN.
DR PRINTS: P00390: PHPLIPASEC.
DR PROSITE: PS00018: EF_HAND; 2.
DR PROSITE: PS00003: PH_DOMAIN; 1.
DR PROSITE: PS50004: C2_DOMAIN; 2; 1.
DR PROSITE: PS50007: PIPLC_X_DOMAIN; 1.
DR PROSITE: PS50008: PIPLC_Y_DOMAIN; 1.
KM Hydrolyase; Lipid degradation; Transducer; Calcium-binding.
FT DOMAIN 21 130
FT FT CA_BIND 153 164
FT FT CA_BIND 189 200
FT DOMAIN 286 440
FT DOMAIN 492 609
FT DOMAIN 616 720
FT ACT_SITE 311 311
FT ACT_SITE 356 356
SO SEQUENCE 756 AA: 85763 MW: AD9AA251C5BADF8 CRC64;

Query Match 64.5%; Score 40; DB 1; Length 756;
Best Local Similarity 66.7%; Pred. No. 27;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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QY 3 GYSXPSPG 11
1:11111
DB 506 GRSSPCTPG 514

RESULT 12

RSCC_RAT STANDARD: PRT: 1387 AA.

AC 008774; 088383;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE REGULATOR OF G-PROTEIN SIGNALING 12 (RGS12).
GN RGS12.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN;
RX MEDLINE; 97312490.
RA Snow B.E., Antonio L., Suggs S., Gutstein H.B., Siderovski D.P.,
RT "Molecular cloning and expression analysis of rat Rgs12 and Rgs14,"
RL Biochem. Biophys. Res. Commun. 233:770-777(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN;
RX MEDLINE; 98316347.
RA Snow B.E., Hall R.A., Kruminis A.M., Brothers G.M., Bouchard D.,
RT Brothers C.A., Chung S., Mangion J., Gilman A.G., Lefkowitz R.J.,
RA Siderovski D.P.;
RT "GTPase activating specificity of RGS12 and binding specificity of an
alternatively spliced PDZ (PSD-95/Dlg/ZO-1) domain.";
RL J. Biol. Chem. 273:17749-17755(1998).
CC -1- FUNCTION: INHIBITS SIGNAL TRANSDUCTION BY INCREASING THE GTPASE
ACTIVITY OF G PROTEIN ALPHA SUBUNITS THEREBY DRIVING THEM INTO
THEIR INACTIVE GDP-BOUND FORM.
CC -1- ALTERNATIVE PRODUCTS: THERE ARE AT LEAST TWO ISOFORMS THAT ARISE
FROM ALTERNATIVE SPLICING.
CC -1- TISSUE SPECIFICITY: EXPRESSED AT HIGH LEVELS IN BRAIN AND LUNG AND
AND LOWER LEVELS IN TESTIS, HEART, AND SPLEEN.
CC -1- SIMILARITY: BELONGS TO THE RGS FAMILY.
CC -1- SIMILARITY: CONTAINS 1 PDZ DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 PDZ DOMAIN.
CC -----
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or send an email to license@isb-sib.ch).
CC -----
DR EMBL: U92280; AAC53176.1;
DR EMBL: A035151; AAC40154.1;
DR HSSP: P49799; IAGR.
DR PFAM: PF00595; PDZ; 1.
DR PFAM: PF00615; RGS; 1.
DR PROSITE: PS01179; PID; 1.
KM Signal transduction inhibitor: Alternative splicing.
FT DOMAIN 21 97 PDZ.
FT DOMAIN 227 339 PID.
FT DOMAIN 715 832 RGS.
FT DOMAIN 1368 1373 POLY-PRO.
FT VARSPIC 1 648 MISSING (IN ISOFORM PDZ-LESS).
FT VARSPIC 649 666 SFGSRRESFLTRSDIDE -> MNLEKGLSDSDVFIQQ
(IN ISOFORM PDZ-LESS)
SQ SEQUENCE 1387 AA: 150468 MW: 958047D106B08310 CACG64:

QY 2 SGXSPGSPGT 12
1:11111
DB 1294 SAHSTPGPPT 1304

RESULT 13

CA14_CAEEL STANDARD: PRT: 1758 AA.

AC P17139;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE COLLAGEN ALPHA 1(IV) CHAIN PRECURSOR.
GN EMB-9 OR CLB-2 OR K0A44.1.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Peloderinae; Caenorhabditis.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RX MEDLINE; 91141582;
RA Guo X., Johnson J.J., Kramer J.M.;
RT "Embryonic lethality caused by mutations in basement membrane
collagen of C. elegans.";
RL Nature 349:707-709(1991).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RX MEDLINE; 94150718.
RA Wilson R., Almscough R., Anderson K., Baynes C., Barks M.,
RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
RA Craxton M., Dear S., Du Z., Durbin R., Favell A., Fraser A.,
RA Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,
RA Johnston L., Jones K., Kershaw J., Kirsten J., Laister N.,
RA Latreille P., Lightning J., Lloyd C., Mottimore B., O'Callaghan M.,
RA Parsons J., Percy C., Rifkin L., Roopra A., Saunders D., Shownkeen R.,
RA Sims M., Smalton N., Smith A., Smith M., Sonhammer E., Staden R.,
RA Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K.,
RA Watson R., Watson A., Welstock L., Wilkinson-Spoat J.,
RA Wohlschlag P.;
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
elegans.";
RL Nature 368:32-38(1994).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RX MEDLINE; 90008929.
RA Guo X., Kramer J.M.;
RT "The two Caenorhabditis elegans basement membrane (type IV) collagen
genes are located on separate chromosomes.";
RL J. Biol. Chem. 264:17574-17582(1989).
CC -1- SUBUNIT: TRIMERS OF TWO ALPHA 1(IV) AND ONE ALPHA 2(IV) CHAIN.
CC -1- TYPE IV COLLAGEN FORMS A MESH-LIKE NETWORK LINKED THROUGH
INTERMOLECULAR INTERACTIONS BETWEEN 7S DOMAINS AND BETWEEN NC1
DOMAINS.
CC -1- DOMAIN: ALPHA CHAINS OF TYPE IV COLLAGEN HAVE A NONCOLLAGENOUS
DOMAIN (NC1) AT THEIR C-TERMINUS, FREQUENT INTERRUPTIONS OF THE
G-X-Y REPEATS IN THE LONG CENTRAL TRIPLE-HELICAL DOMAIN (WHICH MAY
CAUSE FLEXIBILITY IN THE TRIPLE HELIX), AND A SHORT N-TERMINAL
TRIPLE-HELICAL 7S DOMAIN.
CC -1- PTM: PROLINES AT THE THIRD POSITION OF THE TRIPEPTIDE REPEATING
UNIT (G-X-Y) ARE HYDROXYLATED IN SOME OR ALL OF THE CHAINS.
CC -1- PTM: TYPE IV COLLAGENS CONTAIN NUMEROUS CYSTEINE RESIDUES WHICH
ARE INVOLVED IN INTER- AND INTRAMOLECULAR DISULFIDE BONDING. 12 OF
THESE, LOCATED IN THE NC1 DOMAIN, ARE CONSERVED IN ALL KNOWN TYPE
IV COLLAGENS.
CC -1- DISEASE: MUTATIONS IN THIS GENE CAUSE TEMPERATURE-SENSITIVE
LETHALITY DURING LATE EMBRYOGENESIS.
CC -----
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DR EMBL; X56979; CA440299.1; -;
 DR EMBL; Z27078; CA81584.1; -;
 DR EMBL; J05067; AAB59179.1; -;
 DR PIR; B34476; B34476.
 DR PIR; S13651; S13651.
 DR WORMPEP; K04H4.1; CE00246.
 DR PFM; PF01413; C4; 2.
 DR PFM; PF01391; Collagen; 22.
 KW Extracellular matrix; Connective tissue; Basement membrane;
 KW Repeat; Hydroxylation; Glycoprotein; Collagen; Signal.

FT PROPEP 1 2194 AMINO-TERMINAL PROPEPTIDE (7S DOMAIN).
 FT CHAIN 7195 1758 COLLAGEN ALPHA 1(IV) CHAIN.
 FT DOMAIN 195 1529 TRIPLE-HELICAL REGION.
 FT DISULFID 1530 1758 NONHELICAL REGION (NC1).
 FT DISULFID 1549 1640 OR 1637 (BY SIMILARITY).
 FT DISULFID 1582 1637 OR 1640 (BY SIMILARITY).
 FT DISULFID 1594 1600 BY SIMILARITY.
 FT DISULFID 1659 1754 OR 1751 (BY SIMILARITY).
 FT DISULFID 1693 1751 OR 1754 (BY SIMILARITY).
 FT VARIANT 1705 1711 BY SIMILARITY.
 FT VARIANT 402 402 G -> E (IN MUTANT G34).
 FT VARIANT 408 408 G -> E (IN MUTANT G23/HG70).
 FT CONFLICT 1514 1514 P -> O (IN REF. 3).
 FT CONFLICT 130 185 GFGPMGLAGPGGSGNGNGRGLSGPGEAGGNGR
 FT KGVGSGRSRSGPGLP -> VSDLSKSPICHTHLSVYS
 FT VLRLSECPDLDDQGNLDKTDGDDQSPDHKEVSIH
 FT KDARELKENEDQEFQVQ (IN REF. 2).
 FT PVGPA -> ISDQV (IN REF. 2).
 FT CONFLICT 259 263 LDN -> AGOR (IN REF. 2).
 FT CONFLICT 302 304 MISSING (IN REF. 2).
 FT CONFLICT 366 404 G -> R (IN REF. 2).
 FT CONFLICT 581 581 P -> R (IN REF. 2).
 FT CONFLICT 768 768 PG -> TR (IN REF. 2).
 FT CONFLICT 813 814 D -> V (IN REF. 2).
 FT CONFLICT 830 830 P -> T (IN REF. 2).
 FT CONFLICT 1275 1275 P -> L (IN REF. 2).
 FT CONFLICT 1722 1722 P -> L (IN REF. 2).
 FT SEQUENCE 1758 AA; 170857 MW; 7083D9AF65E0D45 CRC64;

Query Match 64.5%; Score 40; DB 1; Length 1758;
 Best Local Similarity 66.7%; Pred. No. 62;
 Matches 8; Conservative 2; Mismatches 0; Indels 2; Gaps 1;

OY 1 KSGYSXPGSPGT 12
 Db 1474 KAGY--PCAPGT 1483

RESULT 14
 CA24_CAEEL STANDARD; PRT; 1758 AA.
 ID CA24_CAEEL
 AC P17140;
 DT 01-AUG-1990 (Rel. 15, Created)
 DT 01-OCT-1994 (Rel. 30, Last sequence update)
 DT 15-FEB-2000 (Rel. 39, Last annotation update)
 DE COLLAGEN ALPHA 2(IV) CHAIN PRECURSOR.
 GN LEP-2 OR CLB-1.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RX MEDLINE; 94012964.
 RA Sibley M.H., Johnson J.J., Mello C.C., Kramer J.M.;
 RT "Genetic identification, sequence, and alternative splicing of the

RT Caenorhabditis elegans alpha 2(IV) collagen gene.";
 RL J. Cell Biol. 123:355-264(1993).
 RN [2]
 RP PRELIMINARY SEQUENCE OF 1495-1758 FROM N.A.
 RC STRAIN-BRISTOL N2;
 RX MEDLINE; 90008929.
 RA Guo X., Kramer J.M.;
 RT "The two Caenorhabditis elegans basement membrane (type IV) collagen
 RT genes are located on separate chromosomes.";
 RL J. Biol. Chem. 264:17574-17582(1989).
 RN [3]
 RP VARIANTS.
 RX MEDLINE; 94320591.
 RA Sibley M.H., Graham P.L., von Mendel N., Kramer J.M.;
 RT "Mutations in the alpha 2(IV) basement membrane collagen gene of
 RT Caenorhabditis elegans produce phenotypes of differing severities.";
 RL EMO J. 13:3278-3285(1994).
 CC -1- FUNCTION: COLLAGEN TYPE IV IS SPECIFIC FOR BASEMENT MEMBRANES.
 CC -1- SUBUNIT: TRIMERS OF TWO ALPHA 1(IV) AND ONE ALPHA 2(IV) CHAIN.
 CC TYPE IV COLLAGEN FORMS A MESH-LIKE NETWORK LINKED THROUGH
 CC INTERMOLECULAR INTERACTIONS BETWEEN 7S DOMAINS AND BETWEEN NC1
 CC DOMAINS.
 CC -1- ALTERNATIVE PRODUCTS: TWO ISOFORMS; I (SHOWN HERE) AND II; ARE
 CC PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- TISSUE SPECIFICITY: FORM I IS PREDOMINANT IN EMBRYOS AND FORM
 CC II IS PREDOMINANT IN THE LARVAE AND ADULTS.
 CC -1- DOMAIN: ALPHA CHAINS OF TYPE IV COLLAGEN HAVE A NONCOLLAGENOUS
 CC DOMAIN (NC1) AT THEIR C-TERMINUS, FREQUENT INTERRUPTIONS OF THE
 CC G-X-Y REPEATS IN THE LONG CENTRAL TRIPLE-HELICAL DOMAIN (WHICH MAY
 CC CAUSE FLEXIBILITY IN THE TRIPLE HELIX), AND A SHORT N-TERMINAL
 CC TRIPLE-HELICAL 7S DOMAIN.
 CC -1- PTM: PROLINES AT THE THIRD POSITION OF THE TRIPETIDE REPEATING
 CC UNIT (G-X-Y) ARE HYDROXYLATED IN SOME OR ALL OF THE CHAINS.
 CC -1- PTM: TYPE IV COLLAGENS CONTAIN NUMEROUS CYSTEINE RESIDUES WHICH
 CC ARE INVOLVED IN INTER- AND INTRAMOLECULAR DISULFIDE BONDING. 12 OF
 CC THESE, LOCATED IN THE NC1 DOMAIN, ARE CONSERVED IN ALL KNOWN TYPE
 CC IV COLLAGENS.
 CC -1- DISEASE: MUTATIONS IN LEP-2 ARE GENERALLY EMBRYONIC LETHAL.
 CC
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DR EMBL; Z22964; CA80536.1; -;
 DR EMBL; Z22964; CA80537.1; -;
 DR EMBL; J05066; AAA27989.1; -;
 DR EMBL; U22327; AAA64312.1; ALT-SEQ.
 DR PIR; A34476; A34476.
 DR PFM; PF01413; C4; 2.
 DR PFM; PF01391; Collagen; 23.
 KW Hydroxylation; Connective tissue; Basement membrane; Repeat; Collagen;
 KW Alternative splicing; Glycoprotein; Signal.

FT SIGNAL 1 26
 FT CHAIN 27 1758
 FT DOMAIN 27 42
 FT DOMAIN 42 1527
 FT DOMAIN 1528 1758
 FT DISULFID 1546 1635
 FT DISULFID 1579 1632
 FT DISULFID 1591 1597
 FT DISULFID 1654 1750
 FT DISULFID 1688 1747
 FT DISULFID 1700 1707
 FT CARBOHYD 248 248
 FT VARIANT 48 48
 FT VARIANT 366 366
 FT VARIANT 570 570
 FT VARIANT 588 588
 FT VARIANT 597 597

G -> E (IN MN114; 73% LETHAL).
 A -> T (IN MN126; 100% LETHAL).
 G -> E (IN MN109; 37% LETHAL).
 G -> R (IN MN103 AND MN151; 96% LETHAL).
 G -> R (IN MN152; 50% LETHAL).


```

FT  VARIANT  690  690  G -> R (IN MN101; 100% LETHAL).
FT  VARIANT  690  690  G -> E (IN MN129; 100% LETHAL).
FT  VARIANT  737  737  G -> E (IN MN143; 100% LETHAL).
FT  VARIANT  877  877  G -> R (IN G30; 90% LETHAL).
FT  VARIANT  904  904  G -> R (IN E1470; 94% LETHAL).
FT  VARIANT  1003  1003  G -> E (IN MN139; 20% LETHAL).
FT  VARIANT  1125  1125  G -> D (IN G25; 2% LETHAL).
FT  VARIANT  1152  1152  G -> D (IN MN147; 7% LETHAL).
FT  VARIANT  1286  1286  G -> D (IN G37 AND B246; 9% LETHAL).
FT  VARIANT  229  264  GDGSGVPPGPPGPGTIGSGIVGRNGPKGK (IN
FT  VARSPLIC 229  264  DIGAMGPAGPPGPIATMSKGTIIGPKGDLGKGEK (IN
FT  P -> L (IN REF. 1).
FT  ISOFORM II).
SQ  CONFLICT  1682  1682  P -> L (IN REF. 1).
SQ  SEQUENCE  1758 AA; 167750 MW; 97EE3F3DBB2D2AC5 CRC64;

```

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Query Match      64.5%; Score 40; DB 1; Length 1758;
Best Local Similarity 54.5%; Pred. No. 62;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

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OY  1 KSGYXPGSPG 11
    :||| |||
Db  680 EAGYGQPG 690

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RESULT 15
ACCC_ANASP STANDARD; PRT; 447 AA.
AC 006862;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 01-FEB-1995 (Rel. 31, Last annotation update)
DE BIOTIN CARBOXYLASE (EC 6.3.4.14) (A SUBUNIT OF ACETYL-COA
DE CARBOXYLASE (EC 6.4.1.2)) (ACC).
GN ACCC.
OS Anabaena sp. (strain PCC 7120).
OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Anabaena.
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE; 93352435.
RA Gornicki P., Scarpino L.A., Haselkorn R.;
RT *Genes for two subunits of acetyl coenzyme A carboxylase of Anabaena
RT sp. strain PCC 7120: biotin carboxylase and biotin carboxyl carrier
RT protein."
RL J. Bacteriol. 175:5268-5272(1993).
CC -1- FUNCTION: THIS PROTEIN IS A COMPONENT OF THE ACETYL COENZYME A
CC CARBOXYLASE COMPLEX; FIRST, BIOTIN CARBOXYLASE CATALYZES THE
CC CARBOXYLATION OF THE CARRIER PROTEIN AND THEN THE TRANSCARBOXYLASE
CC TRANSFERS THE CARBOXYL GROUP TO FORM MALONYL-COA.
CC -1- CATALYTIC ACTIVITY: ATP + BIOTIN-CARBOXYL-CARRIER PROTEIN + CO(2)
CC - ADP + ORTHOPHOSPHATE + CARBOXYBIOTIN-CARBOXYL-CARRIER PROTEIN.
CC -1- PATHWAY: FIRST STEP IN LONG-CHAIN FATTY ACID SYNTHESIS.
CC -1- SUBUNIT: ACETYL-COA CARBOXYLASE IS AN HETEROHOMER OF BIOTIN
CC CARBOXYL CARRIER PROTEIN, BIOTIN CARBOXYLASE AND THE TWO SUBUNITS
CC OF CARBOXYL TRANSFERASE IN A 2:2 COMPLEX.
CC -1- SIMILARITY: TO OTHER BIOTIN-DEPENDENT ENZYMES AND CARBOXYL-
CC PHOSPHATE SYNTHETASES.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: L14862; AAB51770.1; -
CC RSP; P24182; 1BNC.
CC PFAM: PF00289; CPSase_1_chain; 1.
CC PROSITE: PS00866; CPSASE_1; 1.
CC PROSITE: PS00867; CPSASE_2; 1.
CC Fatty acid biosynthesis; Lysase; Biotin; ATP-binding.
FT NP_BIND 163 168 ATP (BY SIMILARITY).

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FT ACT_SITE 293 293 BY SIMILARITY.
SQ SEQUENCE 447 AA; 49104 MW; 8A541B38B39E0F9 CRC64;

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Query Match      62.9%; Score 39; DB 1; Length 447;
Best Local Similarity 70.0%; Pred. No. 23;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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OY  2 SGYXPGSPG 11
    ||| |||
Db  357 SGYLPGGPG 366

```

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Search completed: October 2, 2000, 18:43:36
UD time: 2483 sec

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GenCore version 4.5
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OW protein - protein search, using sw model

Run on: October 2, 2000, 17:34:39 ; Search time 162.96 Seconds
(without alignments)
5.106 Million cell updates/sec

Title: US-09-142-613-2
Perfect score: 62
Sequence: 1 KSGXSXPSPCT 12

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 225878 seqs, 69334122 residues
Total number of hits satisfying chosen parameters: 225878

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: SPTREMBL.12.*
1: sp.archaea:*
2: sp.bacteria:*
3: sp.fungi:*
4: sp.human:*
5: sp.invertebrate:*
6: sp.mammal:*
7: sp.mhc:*
8: sp.organelle:*
9: sp.phage:*
10: sp.plant:*
11: sp.recent:*
12: sp.virus:*
13: sp.vertebrate:*
14: sp.unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	58	93.5	316	6	Q28189
2	58	93.5	338	6	Q28190
3	58	93.5	347	6	Q28188
4	58	93.5	350	11	Q60686
5	58	93.5	365	6	Q28186
6	58	93.5	369	6	Q28185
7	58	93.5	372	11	Q60685
8	58	93.5	374	11	Q63677
9	58	93.5	402	6	Q02828
10	58	93.5	416	6	Q28187
11	58	93.5	430	11	Q60684
12	58	93.5	686	11	Q63567
13	58	93.5	295	5	Q17939
14	58	93.5	295	5	Q17939
15	43	69.4	553	5	Q93367
16	42	67.7	1149	12	Q9WB08
17	42	67.7	1457	12	Q9WB04
18	42	67.7	1457	12	Q9WB04
19	42	67.7	1463	12	Q9YN01

20	41	66.1	126	11	Q9WV05
21	41	66.1	258	2	Q32502
22	41	66.1	755	4	Q00261
23	41	66.1	1742	5	Q24463
24	41	66.1	1802	5	Q17163
25	41	66.1	6658	5	Q76281
26	40	64.5	1345	1	Q54437
27	40	64.5	1758	5	Q19098
28	40	64.5	1759	5	Q19099
29	39	62.9	313	10	Q82020
30	39	62.9	1752	5	Q07265
31	39	62.9	2606	5	Q21920
32	38	61.3	290	10	Q80945
33	38	61.3	455	6	Q28495
34	38	61.3	462	4	Q15039
35	38	61.3	480	3	Q9Y798
36	38	61.3	539	4	Q9Y186
37	38	61.3	625	11	Q88991
38	38	61.3	641	3	Q9Y879
39	38	61.3	752	5	Q94814
40	38	61.3	778	4	Q14639
41	37	59.7	95	5	Q17137
42	37	59.7	264	1	Q9Y8K5
43	37	59.7	285	2	Q69997
44	37	59.7	323	6	Q28869
45	37	59.7	346	13	Q93404

ALIGNMENTS

RESULT 1
Q28189 PRELIMINARY; PRT; 316 AA.
ID Q28189
AC Q28189
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DI 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DE 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
TAU PROTEIN.
GN TAU.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia;
OC Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 89261765.
RA HIMMLER A., DRECHSEL D., KIRSCHNER M.W., MARTIN D.W.;
RT "Tau consists of a set of proteins with repeated C-terminal
microtubule-binding domains and variable N-terminal domains.";
RL Mol. Cell. Biol. 9:1381-1388(1989).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE; 89261766.
RA HIMMLER A.;
RT "Structure of the bovine tau gene: alternatively spliced transcripts
generate a protein family";
RL Mol. Cell. Biol. 9:1389-1396(1989).
DR EMBL; M26178; AA51606.1;
DR EMBL; L34940; AA51606.1; JOINED.
DR EMBL; L34941; AA51606.1; JOINED.
DR EMBL; L34944; AA51606.1; JOINED.
DR EMBL; L34946; AA51606.1; JOINED.
DR EMBL; L34948; AA51606.1; JOINED.
DR EMBL; L34950; AA51606.1; JOINED.
DR EMBL; L34951; AA51606.1; JOINED.
DR PROSITE; PS00429; TAU_MAP; 3.
DR Pfam; PF00418; tubulin-binding; 3.
KW Microtubules; Repeat.
SQ SEQUENCE 316 AA; 32770 MW; DEC3A429 CRC32;

Query Match 93.5%; Score 58; DB 6; Length 316;

Best Local Similarity 83.3%; Pred. No. 0.014;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 KSGYXPGSPGT 12
:|||||
DB 132 RSGYSSPGSPGT 143

RESULT 2

ID 028190 PRELIMINARY; PRT; 338 AA.
AC 028190;
DT 01-NOV-1996 (TREMBLREL. 01, Created)
DT 01-NOV-1996 (TREMBLREL. 01, Last sequence update)
DE 01-NOV-1999 (TREMBLREL. 12, Last annotation update)
DE TAU PROTEIN.
GN TAU.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae;
OC Bovinae; Bos.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 89261765.
RA HIMLER A., DRECHSEL D., KIRSCHNER M.W., MARTIN D.W.;
RT "tau consists of a set of proteins with repeated C-terminal
microtubule-binding domains and variable N-terminal domains."
RL Mol. Cell. Biol. 9:1381-1388(1989).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE; 89261766.
RA HIMLER A.;
RT "Structure of the bovine tau gene: alternatively spliced transcripts
generate a protein family."
RL Mol. Cell. Biol. 9:1389-1396(1989).
DR EMBL; M26178; AAA51603.1; JOINED.
DR EMBL; L34940; AAA51603.1; JOINED.
DR EMBL; L34941; AAA51603.1; JOINED.
DR EMBL; L34943; AAA51603.1; JOINED.
DR EMBL; L34944; AAA51603.1; JOINED.
DR EMBL; L34946; AAA51603.1; JOINED.
DR EMBL; L34948; AAA51603.1; JOINED.
DR EMBL; L34950; AAA51603.1; JOINED.
DR EMBL; L34951; AAA51603.1; JOINED.
DR PROSITE; PS00229; TAU_MAP; 3.
DR PFM; PF00418; tubulin-binding; 3.
KM Microtubules; Repeat.
SQ SEQUENCE 338 AA; 34965 MW; F349F977 CRC32;

Query Match 93.5%; Score 58; DB 6; Length 338;
Best Local Similarity 83.3%; Pred. No. 0.015;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 KSGYXPGSPGT 12
:|||||
DB 154 RSGYSSPGSPGT 165

RESULT 3

ID 028188 PRELIMINARY; PRT; 347 AA.
AC 028188;
DT 01-NOV-1996 (TREMBLREL. 01, Created)
DT 01-NOV-1996 (TREMBLREL. 01, Last sequence update)
DE 01-NOV-1999 (TREMBLREL. 12, Last annotation update)
DE TAU PROTEIN.
GN TAU.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae;
OC Bovinae; Bos.
RN [1]

RP SEQUENCE FROM N.A.
RX MEDLINE; 89261765.
RA HIMLER A., DRECHSEL D., KIRSCHNER M.W., MARTIN D.W.;
RT "tau consists of a set of proteins with repeated C-terminal
microtubule-binding domains and variable N-terminal domains."
RL Mol. Cell. Biol. 9:1381-1388(1989).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE; 89261766.
RA HIMLER A.;
RT "Structure of the bovine tau gene: alternatively spliced transcripts
generate a protein family."
RL Mol. Cell. Biol. 9:1389-1396(1989).
DR EMBL; M26178; AAA51605.1; JOINED.
DR EMBL; L34940; AAA51605.1; JOINED.
DR EMBL; L34941; AAA51605.1; JOINED.
DR EMBL; L34944; AAA51605.1; JOINED.
DR EMBL; L34946; AAA51605.1; JOINED.
DR EMBL; L34948; AAA51605.1; JOINED.
DR EMBL; L34949; AAA51605.1; JOINED.
DR EMBL; L34950; AAA51605.1; JOINED.
DR EMBL; L34951; AAA51605.1; JOINED.
DR PROSITE; PS00229; TAU_MAP; 4.
DR PFM; PF00418; tubulin-binding; 4.
KM Microtubules; Repeat.
SQ SEQUENCE 347 AA; 36016 MW; 00FD6406 CRC32;

Query Match 93.5%; Score 58; DB 6; Length 347;
Best Local Similarity 83.3%; Pred. No. 0.015;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 KSGYXPGSPGT 12
:|||||
DB 132 RSGYSSPGSPGT 143

RESULT 4

ID 060686 PRELIMINARY; PRT; 350 AA.
AC 060686;
DT 01-NOV-1996 (TREMBLREL. 01, Created)
DT 01-NOV-1996 (TREMBLREL. 01, Last sequence update)
DE 01-NOV-1999 (TREMBLREL. 12, Last annotation update)
DE MICROTUBULE-ASSOCIATED PROTEIN TAU ISOFORM 5.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-HIM OPL SPF; TISSUE-LIVER;
RA KENNER L., EFFERL R., ZATLOUKAL K., HOEPLER G., DENK H.;
RL Submitted (AUG-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; U12916; AAA58345.1; JOINED.
DR PROSITE; PS00229; TAU_MAP; 4.
DR PFM; PF00418; tubulin-binding; 4.
KM Microtubules; Repeat.
SQ SEQUENCE 350 AA; 36740 MW; 9C54BC5E CRC32;

Query Match 93.5%; Score 58; DB 11; Length 350;
Best Local Similarity 83.3%; Pred. No. 0.015;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 KSGYXPGSPGT 12
:|||||
DB 103 RSGYSSPGSPGT 114

RESULT 5

ID 028186 PRELIMINARY; PRT; 365 AA.
AC 028186;

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DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)
DE TAU PROTEIN.
GN TAU.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae;
OC Bovinae; Bos.
[1]
RN SEQUENCE FROM N.A.
RX MEDLINE: 89261765.
RA HIMLER A., DRECHSEL D., KIRSCHNER M.W., MARTIN D.W.;
RT "tau consists of a set of proteins with repeated C-terminal
RT microtubule-binding domains and variable N-terminal domains.";
RL Mol. Cell. Biol. 9:1381-1388(1989).
[2]
RN SEQUENCE FROM N.A.
RX MEDLINE: 89261766.
RA HIMLER A.;
RT "Structure of the bovine tau gene: alternatively spliced transcripts
RT generate a protein family.";
RL Mol. Cell. Biol. 9:1389-1396(1989).
DR EMBL: M26178; AA51604.1; -.
DR EMBL: L34940; AA51604.1; JOINED.
DR EMBL: L34941; AA51604.1; JOINED.
DR EMBL: L34944; AA51604.1; JOINED.
DR EMBL: L34946; AA51604.1; JOINED.
DR EMBL: L34947; AA51604.1; JOINED.
DR EMBL: L34948; AA51604.1; JOINED.
DR EMBL: L34949; AA51604.1; JOINED.
DR EMBL: L34950; AA51604.1; JOINED.
DR EMBL: L34951; AA51604.1; JOINED.
DR PROSITE: PS00229; TAU_MAP; 4.
DR PFM: PF00418; tubulin-binding; 4.
KW Microtubules; Repeat.
SQ SEQUENCE 365 AA; 37923 MW; 08A4187E CRC32;

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Query Match 93.5%; Score 58; DB 6; Length 365;
Best Local Similarity 83.3%; Pred. No. 0.016;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KSGYXPGSPGT 12
:|||||
DB 150 RSGYSPGSPGT 161

RESULT 6
Q28185 PRELIMINARY; PRT; 369 AA.
AC Q28185;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)
DE TAU PROTEIN.
GN TAU.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae;
OC Bovinae; Bos.
[1]
RN SEQUENCE FROM N.A.
RX MEDLINE: 89261765.
RA HIMLER A., DRECHSEL D., KIRSCHNER M.W., MARTIN D.W.;
RT "tau consists of a set of proteins with repeated C-terminal
RT microtubule-binding domains and variable N-terminal domains.";
RL Mol. Cell. Biol. 9:1381-1388(1989).
[2]
RN SEQUENCE FROM N.A.
RX MEDLINE: 89261766.
RA HIMLER A.;
RT "Structure of the bovine tau gene: alternatively spliced transcripts

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RT generate a protein family.";
RL Mol. Cell. Biol. 9:1389-1396(1989).
DR EMBL: M26178; AA51602.1; -.
DR EMBL: L34840; AA51602.1; JOINED.
DR EMBL: L34843; AA51602.1; JOINED.
DR EMBL: L34844; AA51602.1; JOINED.
DR EMBL: L34846; AA51602.1; JOINED.
DR EMBL: L34848; AA51602.1; JOINED.
DR EMBL: L34849; AA51602.1; JOINED.
DR EMBL: L34850; AA51602.1; JOINED.
DR EMBL: L34951; AA51602.1; JOINED.
DR PROSITE: PS00229; TAU_MAP; 4.
DR PFM: PF00418; tubulin-binding; 4.
KW Microtubules; Repeat.
SQ SEQUENCE 369 AA; 38212 MW; 948F16BD CRC32;

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Query Match 93.5%; Score 58; DB 6; Length 369;
Best Local Similarity 83.3%; Pred. No. 0.016;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KSGYXPGSPGT 12
:|||||
DB 154 RSGYSPGSPGT 165

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RESULT 7
Q60685 PRELIMINARY; PRT; 372 AA.
AC Q60685;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)
DE MICROTUBULE-ASSOCIATED PROTEIN TAU ISOFORM 4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
[1]
RN SEQUENCE FROM N.A.
RX STRAIN-HM OFI SPF; TISSUE-LAYER;
RA KENNER L., EPERL R., ZATLOUKAL K., HOEFLER G., DENK H.;
RL Submitted (AUG-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL: U12915; AA58344.1; -.
DR PROSITE: PS00229; TAU_MAP; 4.
DR PFM: PF00418; tubulin-binding; 4.
KW Microtubules; Repeat.
SQ SEQUENCE 372 AA; 38960 MW; 0CFE657B CRC32;

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Query Match 93.5%; Score 58; DB 11; Length 372;
Best Local Similarity 83.3%; Pred. No. 0.016;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KSGYXPGSPGT 12
:|||||
DB 125 RSGYSPGSPGT 136

RESULT 8
Q63677 PRELIMINARY; PRT; 374 AA.
AC Q63677;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)
DE MICROTUBULE ASSOCIATED PROTEIN.
GN TAU.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
[1]
RN SEQUENCE FROM N.A.

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RC STRAIN-MISTAR: TISSUE-BRAIN;
 RX MEDLINE: 94334997.
 RA SAOBT E., MARK R., BARG J., BEHAR L., GINZBURG I.;
 RT "Complete sequence of 3'-untranslated region of tau from rat central
 nervous system. Implications for mRNA heterogeneity.";
 RL J. Mol. Biol. 241:325-331(1994).
 DR EMBL: X79321; CAA55889.1; -;
 DR PROSITE: PS00229; TAU_MAP; 4.
 DR PFM: PF00418; tubulin-binding; 4.
 KW Microtubules; Repeat.
 SQ SEQUENCE 374 AA; 39117 MW; 79D40664 CRC32;

Query Match 93.5%; Score 58; DB 11; Length 374;
 Best Local Similarity 83.3%; Pred. No. 0.016; Mismatches 1; Indels 0; Gaps 0;
 Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 KSGYXPGSPGT 12
 Db 127 RSGYSPGSPGT 138

RESULT 9
 002828 PRELIMINARY; PRT; 402 AA.
 AC 002828;
 DT 01-JUL-1997 (TREMblrel. 04, Created)
 DT 01-MAY-1999 (TREMblrel. 10, Last sequence update)
 DT 01-MAY-1999 (TREMblrel. 10, Last annotation update)
 DE MICROVUBULE-ASSOCIATED PROTEIN TAU.
 OS Capra hircus (Goat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Euthelia; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae;
 OC Caprinae; Capra.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-BRAIN CORTEX;
 RX MEDLINE: 97012131.
 RA NELSON P.T., STEFANSON K., GULCHER J., SAPER C.B.;
 RT "Molecular evolution of tau protein: Implications for Alzheimer's
 disease.";
 RL J. Neurochem. 67:1622-1632(1996).
 CC -1- FUNCTION: HEAT STABLE PROTEIN WHICH PROMOTES MICROTUBULE ASSEMBLY
 AND STABILITY, AND MIGHT BE INVOLVED IN THE ESTABLISHMENT AND
 MAINTENANCE OF NEURONAL POLARITY. BINDS AND STABILIZES AXONAL
 MICROTUBULES WHICH IS IMPORTANT FOR MAINTAINING AXONAL TRANSPORT
 AND DEFINING THE POLARITY OF A NEURON. AXONAL POLARITY IS
 DETERMINED BY TAU LOCALIZATION (IN THE NEURONAL CELL) IN THE
 DOMAIN OF THE CELL BODY DEFINED BY THE CENTROSOME.
 CC -1- SUBCELLULAR LOCATION: MOSTLY FOUND IN THE AXONS OF NEURONS.
 CC -1- ALTERNATIVE PRODUCTS: AT LEAST TWO DIFFERENT ISOBFORMS, TAU-A AND
 TAU-B (SHOWN HERE); OF TAU ARE PRODUCED BY DEVELOPMENTALLY AND
 TISSUE-SPECIFICALLY CONTROLLED ALTERNATIVE SPLICING. THEY DIFFER
 FROM EACH OTHER BY THE PRESENCE OR ABSENCE OF TWO EXONS/INSERTS,
 ONE CONTAINING THE ADDITIONAL TAU/MAP REPEAT. SHORT FORMS ALLOW
 PLASTICITY OF THE CYTOSKELETON WHEREAS LONGER FORMS MAY
 PREFERENTIALLY PLAY A ROLE IN ITS STABILIZATION.
 CC -1- DOMAIN: THE REPEATED DOMAIN BINDS TO TUBULIN. TYPE I TAU CONTAINS
 THREE REPEATS WHILE TYPE II TAU CONTAINS FOUR REPEATS.
 CC -1- PTM: PHOSPHORYLATION AT VARIOUS SERINE AND THREONINE RESIDUES IN
 S-P OR T-P MOTIFS BY PROLINE-DIRECTED PROTEIN KINASES (CDC2, GSK3)
 (A FEW SITES PER PROTEIN IN INTERPHASE, MORE IN MITOSIS), AND AT
 SERINE RESIDUES IN K-X-G-S MOTIFS BY MAP/MICROTUBULE AFFINITY-
 REGULATING KINASE (MARK).
 CC -1- SIMILARITY: CONTAINS 4 OR 5 TAU/MAP REPEATS, FROM WHICH ONE IS
 APPROXIMATE, DEPENDENT ON THE ISOFORM.
 DR EMBL: S83347; AAB50785.1; -;
 DR PROSITE: PS00229; TAU_MAP; 4.
 DR PFM: PF00418; tubulin-binding; 4.
 KW Microtubules; Repeat; Alternative splicing; Cytoskeleton; Acetylation;
 FT Phosphorylation.
 FT INT_MET 0 0 BY SIMILARITY.
 FT MOD_RES 1 1 ACETYLATION (BY SIMILARITY).

FT REPEAT 213 243 TAU/MAP MOTIF.
 FT REPEAT 244 274 TAU/MAP MOTIF.
 FT REPEAT 275 305 TAU/MAP MOTIF.
 FT REPEAT 306 337 TAU/MAP MOTIF.
 FT DISULFID 252 283 BY SIMILARITY.
 FT MOD_RES 223 223 PHOSPHORYLATION (BY MARK) (POTENTIAL).
 FT MOD_RES 254 254 PHOSPHORYLATION (BY MARK) (POTENTIAL).
 FT MOD_RES 285 285 PHOSPHORYLATION (BY MARK) (POTENTIAL).
 FT MOD_RES 317 317 PHOSPHORYLATION (BY MARK) (POTENTIAL).
 FT VARSPLIC 33 61 MISSING (IN TAU-A).
 FT VARSPLIC 236 266 MISSING (IN TAU-A).
 SQ SEQUENCE 402 AA; 41716 MW; FC1E79AB CRC32;

Query Match 93.5%; Score 58; DB 6; Length 402;
 Best Local Similarity 83.3%; Pred. No. 0.018; Mismatches 1; Indels 0; Gaps 0;
 Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 KSGYXPGSPGT 12
 Db 155 RSGYSPGSPGT 166

RESULT 10
 028187 PRELIMINARY; PRT; 416 AA.
 AC 028187;
 DT 01-NOV-1996 (TREMblrel. 01, Created)
 DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
 DT 01-NOV-1999 (TREMblrel. 12, Last annotation update)
 DE TAU PROTEIN.
 GN TAU.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Euthelia; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae;
 OC Bovinae; Bos.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE: 89261765.
 RX HIMLER A., DRECHSEL D., KIRSCHNER M.W., MARTIN D.W.;
 RT "Tau consists of a set of proteins with repeated C-terminal
 microtubule-binding domains and variable N-terminal domains.";
 RL Mol. Cell. Biol. 9:1381-1388(1989).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC MEDLINE: 89261766.
 RX HIMLER A.;
 RT "Structure of the bovine tau gene: alternatively spliced transcripts
 generate a protein family.";
 RT Mol. Cell. Biol. 9:1389-1396(1989).
 RL EMBL: M26178; AAB51601.1; -;
 DR EMBL: L34940; AAB51601.1; JOINED.
 DR EMBL: L34941; AAB51601.1; JOINED.
 DR EMBL: L34942; AAB51601.1; JOINED.
 DR EMBL: L34943; AAB51601.1; JOINED.
 DR EMBL: L34944; AAB51601.1; JOINED.
 DR EMBL: L34945; AAB51601.1; JOINED.
 DR EMBL: L34947; AAB51601.1; JOINED.
 DR EMBL: L34948; AAB51601.1; JOINED.
 DR EMBL: L34949; AAB51601.1; JOINED.
 DR EMBL: L34950; AAB51601.1; JOINED.
 DR EMBL: L34951; AAB51601.1; JOINED.
 DR PROSITE: PS00229; TAU_MAP; 4.
 DR PFM: PF00418; tubulin-binding; 4.
 KW Microtubules; Repeat.
 SQ SEQUENCE 416 AA; 42848 MW; A57504F7 CRC32;

Query Match 93.5%; Score 58; DB 6; Length 416;
 Best Local Similarity 83.3%; Pred. No. 0.018; Mismatches 1; Indels 0; Gaps 0;
 Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 KSGYXPGSPGT 12

DB 201 RSGYSSPGSPGT 212

RESULT 11

060684 PRELIMINARY; PRT; 430 AA.

AC 060684; 01-NOV-1996 (TREMBLrel. 01, Created)

DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)

DE 01-NOV-1999 (TREMBLrel. 12, Last annotation update)

DR MICROBUTULE-ASSOCIATED PROTEIN TAU ISOFORM 23.

OS Mus musculus (Mouse); Chordata; Vertebrata; Mammalia;

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

GN Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

RP [1]

RC SEQUENCE FROM N.A. TISSUE-LIVER;

RA KENNER L., EFFERT R., ZATLOUTAL K., HOFER G., DENK H.;

RL Submitted (AUG-1994) to the EMBL/GenBank/DBJ databases.

DR EMBL; 012914; AAAS8343.1;

DR PROSITE; PS00229; TAU_MAP; 4.

DR PFAM; PF00418; tubulin-binding; 4.

DR Microtubules; Repeat.

SO SEQUENCE 430 AA; 44893 MW; FD52F55A CRC32;

Query Match 93.5%; Score 58; DB 11; Length 430;

Best Local Similarity 83.3%; Pred. No. 0.019;

Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

DB 183 RSGYSSPGSPGT 194

RESULT 12

063567 PRELIMINARY; PRT; 686 AA.

AC 063567; 01-NOV-1996 (TREMBLrel. 01, Created)

DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)

DE 01-NOV-1999 (TREMBLrel. 12, Last annotation update)

GN BIG TAU.

OS Rattus norvegicus (Rat);

OC Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia;

GN Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

RP [1]

RC SEQUENCE FROM N.A.

RA MEDLINE; 92179305.

DR GOEBERT M., SPILLANTINI M.G., CROWTHER R.A.;

RT Cloning of a big tau microtubule-associated protein characteristic of

the peripheral nervous system.

DR Proc. Natl. Acad. Sci. U.S.A. 89:1983-1987(1992).

DR EMBL; M64156; AAA42204.1;

DR PROSITE; PS00229; TAU_MAP; 4.

DR PFAM; PF00418; tubulin-binding; 4.

DR Microtubules; Repeat.

SO SEQUENCE 686 AA; 71774 MW; 70992021 CRC32;

Query Match 93.5%; Score 58; DB 11; Length 686;

Best Local Similarity 83.3%; Pred. No. 0.031;

Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

DB 439 RSGYSSPGSPGT 450

RESULT 13

017939

PRELIMINARY; PRT; 295 AA.

AC 017939; 01-NOV-1996 (TREMBLrel. 01, Created)

DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)

DE 01-NOV-1999 (TREMBLrel. 12, Last annotation update)

GN C12D8.8 PROTEIN.

OS Caenorhabditis elegans.

OC Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditidae;

GN Rhabditia; Rhabditidae; Rhabditidae; Peloderinae; Caenorhabditis.

RP [1]

RC SEQUENCE FROM N.A.

RA MCMURRAY A.;

RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.

DR [2]

RC SEQUENCE FROM N.A.

RA MEDLINE; 94150718.

RA WILSON R., AINSKOUGH R., ANDERSON K., BAYNES C., BERKS M.,

RA BOWFIELD J., BURTON J., CONNELL M., COPESEY T., COOPER J., COULSON A.,

RA CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,

RA GARDNER A., GREEN P., HARKINS T., HILLIER L., JIER M., JOHNSTON L.,

RA JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,

RA LUTTING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,

RA PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,

RA SMALDON N., SMITH A., SONNHAMMER E., STADEN R., STILSON J.,

RA THERRY-MEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,

RA WATSON A., WEINSTOCK L., WILKINSON-SPROUT J., WOHLDMAN P.,

RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.

RT elegans."

RL Nature 368:32-38(1994).

DR EMBL; 273969; CA98236.1;

DR PFAM; PF01484; Colcuticle.N; 1.

DR PFAM; PF01391; Collagen; 2

SO SEQUENCE 295 AA; 30342 MW; 26A1SEF5 CRC32;

Query Match 71.0%; Score 44; DB 5; Length 295;

Best Local Similarity 63.6%; Pred. No. 3.2;

Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

DB 213 KRGYGAPGAPG 223

RESULT 14

068641 PRELIMINARY; PRT; 435 AA.

AC 068641; 01-AUG-1998 (TREMBLrel. 07, Created)

DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)

DE 01-NOV-1999 (TREMBLrel. 12, Last annotation update)

GN BETA-1,3-GLUCANASE II.

OS Oerskovia xanthineolytica.

OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;

OC Actinomycetales; Micrococcales; Cellulomonadaceae; Oerskovia.

RP [1]

RC SEQUENCE FROM N.A.

RA VENTOM A.M., ASENJO J.A.;

RL Enzyme Microb. Technol. 13:71-75(1991).

DR [2]

RC SEQUENCE FROM N.A.

RA STRAIN-LL G109;

DR MEDLINE; 96409238.

RA PARRADO J., ESCUREDO P.R., CONEJERO-LARA F., KOTIK M., PONTING C.P.,

RT "Molecular characterisation of a thermostable beta-1,3-glucanase from

Oerskovia xanthineolytica."

RT Biochim. Biophys. Acta 1296:145-151(1996).

RL [3]

RP SEQUENCE FROM N.A.

Search completed: October 2, 2000, 18:16:47
 Job time: 2528 sec

RC STRAIN-LL G109;
 RX MEDLINE: 96250169.
 RA FERRER P., HEDGAARD L., HAKTER T., DIERS I., SANVA D., ASENTO J.A.;
 RT "Molecular cloning of a lytic beta-1,3-glucanase gene from Oerskovia
 xanthineolytica LG109. A beta-1,3-glucanase able to selectively
 permeabilize the yeast cell wall."
 RL Ann. N. Y. Acad. Sci. 782:555-566(1996).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN-LL G109;
 RA FERRER P., ANDREWS B.A., ASENTO J.A., HEDGAARD L., DIERS I.;
 RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF052745; AAC38290.1; -
 DR HSSP: P23904; 1AUK.
 DR PROSITE: PS01034; GLYCOSYL_HYDROL_F16; 1.
 DR PFAM: PF00652; Ricin_B_lectin; 1.
 SO SEQUENCE 435 AA; 4697 MW; B7C717E CRC32;

Query Match 71.0%; Score 44; DB 2; Length 435;
 Best Local Similarity 72.7%; Pred. No. 4.8;
 Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 2 SG5XPGSPGT 12
 ||| |||
 DB 294 SG5SPGNPCT 304

RESULT 15
 O93367
 ID O93367 PRELIMINARY; PRT; 553 AA.
 AC O93367;
 DT 01-FEB-1997 (TrEMBLrel. 02, Created)
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
 DT 01-JAN-1999 (TrEMBLrel. 09, Last annotation update)
 DE C4167.3 PROTEIN.
 GN C4167.3.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditidae;
 OC Rhabditina; Rhabditidae; Rhabditidae; Peloderinae; Caenorhabditis.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA STEWARD C.;
 RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 94150718.
 RA WILSON R., AINSOUGH R., ANDERSON K., BAYNES C., BERKS M.,
 RA BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,
 RA CRAYTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
 RA GARDNER A., GREEN P., HAKINS T., HILIER L., JIER M., JOHNSTON L.,
 RA JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
 RA LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
 RA PARSONS J., PERCY C., RIEKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,
 RA SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
 RA THIRRY-MING J., THOMAS K., VAUGHAN K., WATERSTON R.,
 RA WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
 RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
 elegans."
 RL Nature 368:32-38(1994).
 DR EMBL: Z81048; CAB02840.1; -
 SO SEQUENCE 553 AA; 61142 MW; A2548F6C CRC32;

Query Match 69.4%; Score 43; DB 5; Length 553;
 Best Local Similarity 72.7%; Pred. No. 9.2;
 Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 2 SG5XPGSPGT 12
 ||| |||
 DB 323 SG5SPGNPCT 333

Tue Oct 3 09:22:00 2000

us-09-142-613-2.rspt

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: October 2, 2000, 17:32:12 ; Search time 131.89 Seconds
(without alignments)
2.155 Million cell updates/sec

Title: US-09-142-613-2

Perfect score: 62
Sequence: 1 KSGSXSPGSGPT 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 188963 seqs, 23686106 residues

Total number of hits satisfying chosen parameters: 188963

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_36:*

Prod. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	61	98.4	12	1 W34857	Human tau protein
2	58	93.5	34	1 R61330	Peptide phosphoryl
3	58	93.5	34	1 W34875	Human tau protein
4	58	93.5	67	1 R59837	Sequence of human
5	58	93.5	106	1 R92516	Microtubule-associ
6	58	93.5	112	1 R76937	PHF-tau (143-254)
7	58	93.5	352	1 R91294	Paired helical fil
8	58	93.5	352	1 R32708	Human tau-protein.
9	58	93.5	390	1 W05283	Truncated human ta
10	58	93.5	441	1 R58810	Human tau protein.
11	58	93.5	441	1 W05282	Human tau protein.
12	58	93.5	441	1 W34856	Peptide sequence f
13	46	74.2	9	1 R36557	Alzheimer paired h
14	46	74.2	12	1 R38235	Phosphorylated tau
15	46	74.2	12	1 R37554	Oerskovia xanthine
16	44	71.0	263	1 W29455	Oerskovia xanthine
17	44	71.0	435	1 W29456	Oerskovia xanthine
18	39	62.9	13	1 R28237	Phosphopeptide as
19	39	62.9	13	1 W34860	Human tau protein
20	39	62.9	13	1 W34858	Human tau protein
21	39	62.9	234	1 W53973	Pseudomonas fluore
22	39	62.9	303	1 W29457	Oerskovia xanthine
23	39	62.9	447	1 W05207	Anabaena diotin DI
24	39	62.9	447	1 W70402	Anabaena diotin ca
25	39	62.9	448	1 R51080	Biotin carboxylase
26	38	61.3	269	1 R87998	Subtilisin 309 loo
27	38	61.3	286	1 R23924	blac74 mutation (8
28	38	61.3	480	1 W70515	Candida krusei IPC
29	38	61.3	545	1 W28867	Human brain Neurog
30	37	59.7	455	1 R62382	IT10C3, transporte
31	37	59.7	1717	1 W23331	Neuroblastoma indi
32	37	59.7	1831	1 W23329	Microtubule-associ
33	36	58.1	282	1 W34205	Streptomyces trans

34	36	58.1	282	1 W55806	Streptomyces roseo
35	36	58.1	335	1 R25063	Soluble human IL-5
36	36	58.1	335	1 R33699	shIL-5R-alpha, Dec
37	36	58.1	346	1 W00245	Human elav-like ne
38	36	58.1	353	1 R28314	ARSV protein, DNA
39	36	58.1	359	1 R43894	K3. Polypeptide(s)
40	36	58.1	359	1 W00244	Human elav-like ne
41	36	58.1	359	1 W60578	Human neuron-speci
42	36	58.1	396	1 R22216	Sequence of human
43	36	58.1	396	1 R22230	Sequence of secret
44	36	58.1	418	1 R98562	Human neurotensin
45	36	58.1	420	1 R22215	Sequence of human

ALIGNMENTS

RESULT 1
W34857 188963 standard; peptide; 12 AA.
AC W34857:
DE 27-MAR-1998 (first entry)
KW Human tau protein fragment.
KW Antibody; phosphorylated tau protein; paired helical filament;
OS detection; Alzheimer's disease; human.
FH Homo sapiens.
FT Key Location/Qualifiers
FT Modified_site 6 /note= "phosphoserine"
FT PN W09734145-A1.
PD 18-SEP-1997.
PE 13-MAR-1997; J00804.
PR 13-MAR-1996; JP-056090.
PA (MITU) MITSUBISHI CHEM CORP.
PI Imahori K, Ishiguro K, Park J, Sato K, Uchida T;
DR WPI; 97-470978/43.
PT Antibody prepared using a partial peptide containing part of
PT phosphorylated tau protein - used for detecting Alzheimer's disease
PS Example; Page 28; 48pp; Japanese.
CC An antibody, prepared using a partial peptide containing the
CC phosphorylated residue of the phosphorylated tau protein, e.g. the
CC present sequence, in a paired helical filament, can be used to
CC detect Alzheimer's disease, i.e. by detecting phosphorylated tau
CC protein in brain extracts or tissue fragments.
SQ Sequence 12 AA:

Query Match 98.4%, Score 61; DB 1; Length 12;
Best Local Similarity 91.7%; Pred. No. 0.00056;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KSGSXSPGSGPT 12
DB 1 KSGSXSPGSGPT 12

RESULT 2
R61330
AC R61330 standard; Protein; 34 AA.
AC R61330:
DE 24-APR-1995 (first entry)
DE Peptide phosphorylated by human tau-protein kinase.
KW Tau-protein kinase I enzyme; TPK-I; Phosphorylated peptide.
OS Synthetic.
PN EP-616032-A.
PD 21-SEP-1994.
PE 01-MAR-1994; 103057.
PR 02-MAR-1993; JP-041160.
PR 02-MAR-1993; JP-085143.
PR 02-AUG-1993; JP-191246.
PA (TAKA) TAKASHIMA A.
PI (MITU) MITSUBISHI KASEI CORP.
PI Hoshino T, Imahori K, Saito K, Sato S, Shiratsuchi A;

PI Takashima A;
 DR WPI: 94-287181/36.
 PT Newly isolated tau-protein kinase I enzyme - with specificity for
 PT tau-protein providing means for prevention and treatment of
 PT Alzheimer's disease
 PS Example 4; Page 25; 30pp; English.
 CC R61330 is a peptide which has been phosphorylated by human
 CC tau-protein kinase (R61326).
 CC Sequence 34 AA;

Query Match 93.5%; Score 58; DB 1; Length 34;
 Best Local Similarity 83.3%; Pred. No. 0.0047;
 Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 KSGYXSPGSPGT 12
 :|||||
 DB 4 RSGYSSPGSPGT 15

RESULT 3
 W34875
 ID W34875 standard; peptide: 34 AA.
 AC W34875;
 DT 27-MAR-1998 (first entry)
 DE Human tau protein fragment.
 KW Antibody; phosphorylated tau protein; paired helical filament;
 KW detection; Alzheimer's disease; human.
 OS Homo sapiens.
 PN W09734145-A1.
 PD 18-SEP-1997.
 PF 13-MAR-1997; J00804.
 PR 13-MAR-1996; JP-056090.
 RA (MITU) MITSUBISHI CHEM CORP.
 FI Imahori K, Ishiguro K, Park J, Sato K, Uchida T;
 DR WPI: 97-470978/43.
 PT Antibody prepared using a partial peptide containing part of
 PT phosphorylated tau protein - used for detecting Alzheimer's disease
 PS Example; Pages 36-37; 48pp; Japanese.
 CC An antibody, prepared using a partial peptide containing the
 CC phosphorylated residue of the phosphorylated tau protein, e.g. the
 CC present sequence, in a paired helical filament, can be used to
 CC detect Alzheimer's disease, i.e. by detecting phosphorylated tau
 CC protein in brain extracts or tissue fragments.
 CC Sequence 34 AA;

Query Match 93.5%; Score 58; DB 1; Length 34;
 Best Local Similarity 83.3%; Pred. No. 0.0047;
 Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 KSGYXSPGSPGT 12
 :|||||
 DB 4 RSGYSSPGSPGT 15

RESULT 4
 R59837
 ID R59837 standard; peptide: 67 AA.
 AC R59837;
 DT 04-MAR-1995 (first entry)
 DE Sequence of human microtubule-associated protein tau.
 KW Tau protein; brain; cerebral cortex; hydropoma ECACC 92100853;
 KW Alzheimer's disease; monoclonal antibody; paired helical filament.
 OS Homo sapiens.
 PN W09413795-A.
 PD 23-JUN-1994.
 PF 10-DEC-1993; E03499.
 PR 14-DEC-1992; EP-403403.
 RA (INNO-) INNOGENETICS NV SA.
 FI Mercken M, Van De Voorde A, Vandermeeren M, Vanmechelen E;
 DR WPI: 94-234211/28.
 PT Monoclonal antibody reactive with tau protein - used to develop

PT prods. for detection of brain diseases involving tau or paired
 PT helical filaments esp. Alzheimer's disease
 PS Claim 6; Page 38; 52pp; English.
 CC Paired helical filament (PHF) tau was partially purified from
 CC postmortem tissue, consisting mostly of grey matter from the frontal
 CC and temporal cortex obd. from Alzheimer patients. The tissue (5-10g)
 CC was homogenised with 10 vols of cold buffer (10mM Tris, 1mM EGTA,
 CC 0.8M NaCl, 10% sucrose, pH 7.4). After centrifugation for 20 mins at
 CC 4 degrees C, the supernatant was adjusted to 1% (wt/vol) N-
 CC laurylsarcosine and 1% (vol/vol) 2-mercaptoethanol and incubated
 CC while rotating on a mixer for 2.5 hrs at 37 degrees C. The mixt. was
 CC centrifuged at 108,000 g for 35 mins at 20 degrees C. The PHF-tau
 CC pellet was washed with PBS and resuspended in 1ml of the same
 CC buffer. Hybridomas which produced mAbs reactive with tau protein
 CC were obt. from the spleen cells of Balb/C mice primed s.c. with
 CC partially purified PHF. A Mab which forms an immunological complex
 CC with a human tau protein of sequence in R59837 is secreted by the
 CC hybridoma deposited at ECACC on Oct. 8 1992 under No. 92100853.
 CC Sequence 67 AA;

Query Match 93.5%; Score 58; DB 1; Length 67;
 Best Local Similarity 83.3%; Pred. No. 0.0092;
 Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 KSGYXSPGSPGT 12
 :|||||
 DB 40 RSGYSSPGSPGT 51

RESULT 5
 R92516
 ID R92516 standard; peptide: 106 AA.
 AC R92516;
 DT 20-SEP-1996 (first entry)
 DE Microtubule-associated tau protein epitope corresp. to pos. 146-251.
 KW Epitope; microtubule-associated protein; tau; phosphorylation; subclass;
 KW paired helical fibre; neurofibrillary tangle; dementia; neurological;
 KW Alzheimer's disease; monoclonal antibody; brain; pathology.
 OS Synthetic.
 PN W09604309-A1.
 PD 15-FEB-1996.
 PF 31-JUL-1995; E03032.
 PR 29-JUL-1994; EP-870131.
 RA (INNO-) INNOGENETICS NV.
 FI Van DE VOORDE A, Vanmechelen E;
 DR WPI: 96-129358/13.
 PT Monoclonal antibodies specific for phosphorylated tau - for improved
 PT detection and diagnosis of e.g. Alzheimer's Disease
 PS Claim 2; Page 32; 42pp; English.
 CC This is the amino acid of an epitope derived from the microtubule-
 CC associated tau protein. The phosphorylated subclass of tau protein
 CC from which this epitope originates, forms a major part of the paired
 CC helical fibres which make up neurofibrillary tangles seen in patients
 CC suffering from dementia e.g. Alzheimer's disease. The epitope is esp.
 CC isolated from patients who have recently died from Alzheimer's disease.
 CC It is used to generate monoclonal antibodies for the in vitro detection
 CC or diagnosis of brain/neurological diseases such as Alzheimer's disease
 CC or other diseases where neurofibrillary tangles are a pathological
 CC symptom.
 CC Sequence 106 AA;

Query Match 93.5%; Score 58; DB 1; Length 106;
 Best Local Similarity 83.3%; Pred. No. 0.015;
 Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 KSGYXSPGSPGT 12
 :|||||
 DB 49 RSGYSSPGSPGT 60

RESULT 6

R76937
ID R76937 standard; Peptide: 112 AA.
AC R76937;
DE 04-DEC-1995 (first entry)
DE PHF-tau (143-254) peptide.
KW PHF-tau; paired helical filament tau protein; monoclonal antibody;
KW MAb; phosphorylation; neurological disease; Alzheimer disease;
KW cerebrospinal fluid.
OS Homo sapiens.
PN WO9517429-A.
PD 29-JUN-1995.
PF 14-DEC-1994: E04146.
PR 21-DEC-1993: EP-403133.
PA (INNO-) INNOGENETICS NV.
PI Van De Voorde A, Vandermeeren M, Vanmechelen E;
DR WPI: 95-240616/31.
PT Novel monoclonal antibodies specific for abnormally phosphorylated
PT paired helical filament tau protein (PHF-Tau) - useful for post
PT more or in vitro detection of neurological diseases eg. Alzheimer's
PT disease
PT Claim 1: Page 44; 57pp; English.
CC Novel MABs A1180 and A1270 (ECACC 92122204, 93070774) form
CC immunological complexes with a phosphorylated epitope, given in
CC R76937, of abnormally phosphorylated tau protein (PHF-tau). The
CC MABs are used to specifically detect PHF-tau in cerebrospinal fluid.
SQ Sequence 112 AA.

Query Match 93.5%; Score 58; DB 1; Length 112;
Best Local Similarity 83.3%; Pred. No. 0.015;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KSGYXPGSPGT 12
:|||||
DB 52 RSGYSSPGSPGT 63

RESULT 7
ID P91294 standard; protein; 352 AA.
AC P91294;
DE 10-MAR-1993 (revised)
DE 18-DEC-1989 (first entry)
DE Paired helical filament (PHF) core protein.
KW Paired helical filament (PHF) core protein; Alzheimer's disease;
KW neurofibrillary tangles.
OS Homo sapiens
PN WO8903993-A.
PD 05-MAY-1989.
PF 19-OCT-1988; G00867.
PR 19-OCT-1987; GB-024412.
PI (MEDI) Medical Research Council.
PI Wischik CM, Mistein C, Klug A;
DR WPI: 89-150854/20.
PT Paired helical filament core protein - used for providing reagents
PT sensitive to neurofibrillary tangles used for diagnosing Alzheimer's
PT disease.
PT Disclosure; fig 1, 29pp; English.
CC Paired helical filament core protein was sequenced from DNA obtained
CC from brain tissue contg. Alzheimer neurofibrillary tangles. The protein
CC can be used to make MAB's to the PHF core or nucleotide probes, used to
CC diagnose Alzheimer's disease. The protein sequence QIYRKP (AAs 218-223)
CC was also used to design the probes.
CC See also N91707.
SQ Sequence 352 AA;

Query Match 93.5%; Score 58; DB 1; Length 352;
Best Local Similarity 83.3%; Pred. No. 0.048;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KSGYXPGSPGT 12
:|||||

DB 136 RSGYSSPGSPGT 147

RESULT 8
ID R32708 standard; Protein; 352 AA.
AC R32708;
DE 15-JUN-1993 (first entry)
DE Human tau-protein.
KW Alzheimer's disease; diagnosis; subtyping; monitoring; assay.
OS Homo sapiens.
PN WO9303369-A.
PD 18-FEB-1993.
PF 03-AUG-1992: U06382.
PR 01-AUG-1991; US-738778.
PA (VOOR/) VOORHEIS P H.
PI Voorheis PH;
DR WPI: 93-076670/09.
DR N-PSDB: Q37305.
PT Method for diagnosing, subtyping and monitoring Alzheimer's
PT disease - by assaying a sample of body fluid for the presence of a
PT tau-peptide using an anti-tau antibody
PT Disclosure; fig 1; 43pp; English.
CC The sequence is that one form of human tau protein (from Goedert
CC et al., PNAS USA 85: 4051-4055) which was used for the prodn.
CC of anti-tau peptide antibodies. These are used as part of a method
CC for diagnosing, subtyping or monitoring Alzheimer's disease by
CC assaying a sample of body fluid for the presence of a tau-peptide
CC using an anti-tau antibody or the presence of an anti-tau-peptide
CC autoantibody. The methods can be used for confirming a clinical
CC diagnosis of Alzheimer's disease and in following the course of the
CC disease and treatment.
SQ Sequence 352 AA;

Query Match 93.5%; Score 58; DB 1; Length 352;
Best Local Similarity 83.3%; Pred. No. 0.048;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KSGYXPGSPGT 12
:|||||
DB 136 RSGYSSPGSPGT 147

RESULT 9
ID W05283 standard; Protein; 390 AA.
AC W05283;
DE 20-DEC-1996 (first entry)
DE Truncated human tau protein.
KW Tau protein; inhibition; modulation; prophylaxis; treatment;
KW Alzheimer's disease; motor neurone disease; Lewy body disease;
KW progressive supranuclear palsy; Pick's disease.
OS Homo sapiens.
PN WO9630766-A1.
PD 03-OCT-1996.
PF 25-MAR-1996; E01307.
PR 27-MAR-1995; GB-006197.
PI (HOFF) HOFFMANN LA ROCHE & CO AG F.
PI Edwards PC, Harrington CR, Klug A, Roth M, Wischik CM;
DR WPI: 96-45570/45.
PT Assay for inhibitors of tau-tau interaction - used for identifying
PT cpds., partic. phenothiazine cpds., for treating pathological
PT tau-tau or neurofilament aggregation
PT Claim 11; 97pp; English.
CC Detecting an agent which modulates or inhibits tau-tau protein
CC association comprises contacting two tau proteins, distinct from
CC each other yet capable of binding to the other and where one of the
CC tau proteins is labelled, in the presence of the agent suspected of
CC being capable of modulating or inhibiting tau-tau interaction.
CC Agents identified as being modulators or inhibitors of tau-tau
CC interaction may be used for the prophylaxis and treatment of
CC Alzheimer's disease, motor neurone disease, Lewy body disease,

CC Pick's disease or progressive supranuclear palsy. This sequence of
CC the human tau protein is truncated at amino acid residue 390. The
CC full length protein is given in W05282.
SQ Sequence 390 AA;

Query Match 93.5%; Score 58; DB 1; Length 390;
Best Local Similarity 83.3%; Pred. No. 0.053;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 KSGYSPGSPGT 12
Db 194 RSGYSPGSPGT 205

RESULT 10
ID R58810 standard; protein; 441 AA.
AC R58810; 27-MAR-1995 (first entry)
DE Human tau protein.
KW Tau; cerebrospinal fluid; immunosassay; antibody; detection;
KW diagnosis; central nervous system; CNS; cytopathies; cytopathy;
KW Alzheimer's disease.
OS Homo sapiens.
PN W09418560-A.
PD 18-AUG-1994.
PF 10-FEB-1994; J00196.
PR 12-FEB-1993; JP-046133.
PA (TEIJ) TEIJIN LTD
PI Eguichi H, Hosoda K, Kobayashi S, Kubota T, Mori H;
PI Nakamoto T;
DR WPI; 94-279910/34.
PT Sandwich immunosassay of tau protein in cerebrospinal fluid - for
PT diagnosis of Alzheimer's disease and other CNS cytopathies
PS Claim 1; Page 16-18; 36pp; Japanese.
CC Detection of the human tau protein (or fragments of it) in samples
CC of cerebrospinal fluid enables the diagnosis of central nervous
CC system cytopathies such as Alzheimer's disease. Detection is
CC performed using labelled antibodies which recognise sites within the
CC region defined by the amino acid residues 251-441. The antibodies
CC are preferably polyclonal.
SQ Sequence 441 AA;

Query Match 93.5%; Score 58; DB 1; Length 441;
Best Local Similarity 83.3%; Pred. No. 0.06;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 KSGYSPGSPGT 12
Db 194 RSGYSPGSPGT 205

RESULT 11
ID W05282 standard; Protein; 441 AA.
AC W05282;
DT 20-DEC-1996 (first entry)
DE Human tau protein.
KW Tau protein; inhibition; modulation; prophylaxis; treatment;
KW Alzheimer's disease; motor neurone disease; Lewy body disease;
KW progressive supranuclear palsy; Pick's disease.
OS Homo sapiens.
PN W09630766-A1.
PD 03-OCT-1996.
PF 25-MAR-1996; E01307.
PR 27-MAR-1995; GB-006197.
PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
PI Edwards PC, Harrington CR, Kling A, Roth M, Wischik CM;
DR N-PSDB; T39591.
PT Assay for inhibitors of tau-tau interaction - used for identifying

PT cpds, partic. phenothiazine cpds, for treating pathological
PT tau-tau or neuro:fllament aggregation
PS Example 2; Page 53-54; 97pp; English.
CC Detecting an agent which modulates or inhibits tau-tau protein
CC association comprises contacting two tau proteins, distinct from
CC each other yet capable of binding to the other and where one of the
CC tau proteins is labelled, in the presence of the agent suspected of
CC being capable of modulating or inhibiting tau-tau interaction.
CC Agents identified as being modulators or inhibitors of tau-tau
CC interaction may be used for the prophylaxis and treatment of
CC Alzheimer's disease, motor neurone disease, Lewy body disease,
CC Pick's disease or progressive supranuclear palsy.
SQ Sequence 441 AA;

Query Match 93.5%; Score 58; DB 1; Length 441;
Best Local Similarity 83.3%; Pred. No. 0.06;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 KSGYSPGSPGT 12
Db 194 RSGYSPGSPGT 205

RESULT 12
ID W34856 standard; protein; 441 AA.
AC W34856;
DT 27-MAR-1998 (first entry)
DE Human tau protein.
KW Antibody; phosphorylated tau protein; paired helical filament;
KW detection; Alzheimer's disease; human.
OS Homo sapiens.
PN W09734145-A1.
PD 18-SEP-1997.
PF 13-MAR-1997; J00804.
PR 13-MAR-1996; JP-056090.
PA (MTU) MITSUBISHI CHEM CORP.
PI Ihnori K, Ishiguro K, Park J, Sato K, Uchida T;
DR WPI; 97-470978/43.
PT Antibody prepared using a partial peptide containing part of
PT phosphorylated tau protein - used for detecting Alzheimer's disease
PS Claim 2; Pages 25-27; 48pp; Japanese.
CC An antibody prepared using a partial peptide containing the
CC phosphorylated residue of the phosphorylated tau protein, e.g. the
CC present sequence, in a paired helical filament, can be used to
CC detect Alzheimer's disease, i.e. by detecting phosphorylated tau
CC protein in brain extracts or tissue fragments.
SQ Sequence 441 AA;

Query Match 93.5%; Score 58; DB 1; Length 441;
Best Local Similarity 83.3%; Pred. No. 0.06;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 KSGYSPGSPGT 12
Db 194 RSGYSPGSPGT 205

RESULT 13
ID R36557 standard; peptide; 9 AA.
AC R36557;
DT 10-AUG-1993 (first entry)
DE Peptide sequence for abnormally phosphorylated tau protein.
KW Alzheimer's disease; Down's syndrome; Pick's disease; monoclonal;
KW antibody; detection; SSPE; antigen.
OS Synthetic.
FH Key Location/Qualifiers
FT modified_site 3
FT misc_difference 6 /note- "may be phosphorylated"

/note- "may be phosphorylated"

PN W09308302-A.
 PD 29-APR-1993.
 PF 17-OCT-1992; E02392.
 PR 25-OCT-1991; EP-402871.
 PA (INNO-) INNOGENETICS NV SA.
 PI Mandelkow E, Mercken M, Van DE VOORDE A, Vandermeeren M;
 PI Vanmechelen E;
 DR WPI: 93-152493/18.
 PT Monoclonal antibodies binding abnormal micro-tubule-associated
 PT tau-protein - for diagnosing neurological disorders e.g.
 PT Alzheimer's disease, Down syndrome, Pick's disease, etc.
 PS Claim 8; Page 36; 47pp; English.
 CC The peptide is able to form an immunogenic complex with a
 CC monoclonal antibody contg. a phosphorylated epitope of an antigen
 CC belonging to human abnormally phosphorylated tau protein which can be
 CC obtd. from a brain homogenate isolated from the cerebral cortex of a
 CC patient having Alzheimer's disease. The monoclonal antibody is able
 CC to specifically detect only abnormally phosphorylated tau protein and
 CC not react with normal tau protein, and thus may be used in the detection
 CC or diagnosis of neurological diseases, e.g. Alzheimer's disease, Down's
 CC syndrome, Pick's disease or SSPE.
 CC See also R36556.
 CC
 SQ Sequence 9 AA;

Query Match 74.2%; Score 46; DB 1; Length 9;
 Best Local Similarity 88.9%; Pred. No. 1.5e+05;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 YSXGSPGT 12
 |||||
 Db 1 YSPGSPGT 9

RESULT 14
 R38235
 ID R38235 standard; peptide; 12 AA.
 AC R38235;
 DT 08-OCT-1993 (first entry)
 DE Alzheimer paired helical filament tau protein epitope 197-208.
 KW Alzheimer tau protein; phosphorylation-dependent; PHF;
 KW neuronal microtubule; mitogen activated protein kinase; MAP kinase.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT modified_site 3..4
 FT /label- Phosphorylation_motif
 FT modified_site 6..7
 FT /label- Phosphorylation_motif
 FT modified_site 9..10
 FT /label- Phosphorylation_motif
 PN W09311231-A.
 PD 10-JUN-1993.
 PF 07-DEC-1992; E02829.
 PR 06-DEC-1991; EP-120974.
 PR 16-NOV-1992; EP-119551.
 PA (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
 PI Biernat J, Drewes G, Lichtenberg-Kraag B, Mandelkow E;
 PI Steiner B;
 DR WPI: 93-197050/24.
 PT Tau protein epitope(s), specific antibodies and protein kinase(s)
 PT - used in the prevention, diagnosis and treatment of Alzheimer's
 PT disease
 PS Claim 5; Page 89; 148pp; English.
 CC This is one of 26 preferred epitopes which occur in a phosphorylated
 CC state in tau protein from Alzheimer paired helical filaments. The
 CC epitopes all include phosphorylatable serine residues in Ser-Pro
 CC motifs, i.e. Gly-Ser motifs or Cys-Gly-Ser motifs and/or
 CC phosphorylatable threonine residues in Thr-Pro motifs. The pattern
 CC of tau protein phosphorylation differs between Alzheimer's and
 CC non-Alzheimer's individuals. Knowledge of the phosphorylated
 CC epitopes and antibodies which recognise them may be useful in
 CC diagnosis, treatment and prevention of Alzheimer's Disease. The

CC protein kinases present in mammalian brain which phosphorylate the
 CC different epitopes are also claimed but no sequences are given.
 SQ Sequence 12 AA;

Query Match 74.2%; Score 46; DB 1; Length 12;
 Best Local Similarity 88.9%; Pred. No. 0.13;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 YSXGSPGT 12
 |||||
 Db 1 YSPGSPGT 9

RESULT 15
 R37534
 ID R37534 standard; peptide; 12 AA.
 AC R37534;
 DT 07-OCT-1993 (first entry)
 DE Phosphorylated tau protein epitope.
 KW Alzheimer's disease; Alzheimer; paired helical fragments; diagnosis;
 KW treatment; formation; inhibition; inhibitor.
 OS Homo sapiens.
 PN EP-544942-A.
 PD 09-JUN-1993.
 PF 06-DEC-1991; EP-120974.
 PR 06-DEC-1991; EP-120974.
 PA (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
 PI Biernat J, Drewes G, Lichtenberg-Kraag B, Mandelkow EM, Steiner B;
 DR WPI: 93-183841/23.
 PT Phosphorylated tau protein epitope associated with Alzheimer's
 PT disease - is used as protein kinase inhibitor for treatment and
 PT diagnosis
 PS Claim 4; Page 16; 34pp; English.
 CC The sequence is that of an epitope of tau protein which specifically
 CC occurs in a phosphorylated state in tau protein from Alzheimer's
 CC paired helical fragments. It may be used as part of a method for the
 CC in vitro diagnosis and/or monitoring of Alzheimer disease. It may
 CC also be used in an in vitro model for the study of the generation of
 CC the Alzheimer state of proteins and the testing of substances which
 CC prevent the conversion of normal to Alzheimer tau protein. The
 CC epitope occurs at residues 197-208 of human tau protein.
 SQ Sequence 12 AA;

Query Match 74.2%; Score 46; DB 1; Length 12;
 Best Local Similarity 88.9%; Pred. No. 0.13;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 YSXGSPGT 12
 |||||
 Db 1 YSPGSPGT 9

Search completed: October 2, 2000, 18:01:53
 Job time: 1781 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: October 2, 2000, 17:33:18 ; Search time 137.53 seconds
(without alignments)
5.400 Million cell updates/sec

Title: US-09-142-613-2
Perfect score: 62
Sequence: 1 KSGYSXPGSPGT 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 178050 seqs, 61884766 residues

Total number of hits satisfying chosen parameters: 178050

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

PIR64:*
1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	58	93.5	316	1 ORHUT2	microtubule-associ
2	58	93.5	341	2 B28820	microtubule-associ
3	58	93.5	364	2 A28820	microtubule-associ
4	58	93.5	374	2 S46264	microtubule-associ
5	58	93.5	402	1 ORHUT2	microtubule-associ
6	58	93.5	432	2 JS0306	microtubule-associ
7	58	93.5	441	1 ORHUT1	microtubule-associ
8	58	93.5	448	1 ORHUT1	microtubule-associ
9	58	93.5	686	2 A38235	microtubule-associ
10	58	93.5	733	2 A45301	microtubule-associ
11	44	71.0	295	2 T19220	hypothetical prote
12	44	71.0	315	2 T43928	reductase-like pro
13	43	69.4	351	2 A75621	Tors-related prote
14	43	69.4	553	2 T19894	hypothetical prote
15	42	67.7	1986	2 S28353	probable polyketid
16	41	66.1	178	2 A39762	collagen alpha 1(X
17	41	66.1	330	2 S46657	collagen alpha 1(X
18	41	66.1	515	2 H75589	aldenhyde dehydrog
19	41	66.1	641	2 A42019	tyrosine-tRNA lig
20	41	66.1	963	2 T19140	hypothetical prote
21	41	66.1	1742	2 S24600	projectin - fruit
22	41	66.1	6658	2 T13931	projectin - fruit
23	40	64.5	680	2 S31216	collagen alpha 1(X
24	40	64.5	756	2 A35943	phospholipase C (E
25	40	64.5	1345	3 T29090	surface layer asso
26	40	64.5	1387	2 JC5502	G-protein signalin
27	40	64.5	1744	2 S40991	collagen alpha 1(I
28	40	64.5	1758	2 T29350	hypothetical prote
29	40	64.5	1759	2 T29351	collagen alpha 2(I

30	39	62.9	313	2 T09670	abscisic acid acti
31	39	62.9	447	2 A53311	biotin carboxylase
32	39	62.9	511	2 S10527	endoglucanase B pr
33	39	62.9	828	1 D39142	outer membrane ush
34	39	62.9	1752	2 A45407	collagen alpha 3(I
35	39	62.9	2584	2 T24158	hypothetical prote
36	39	62.9	2606	2 T24157	hypothetical prote
37	38	61.3	272	2 T36770	probable expressio
38	38	61.3	290	2 T02543	aldenhyde dehydrog
39	38	61.3	680	1 CGHUID	collagen alpha 1(X
40	38	61.3	870	2 T30110	hypothetical prote
41	37	59.7	95	2 S47600	homeotic protein H
42	37	59.7	264	2 E72642	hypothetical prote
43	37	59.7	285	2 T35195	probable serine pr
44	37	59.7	323	2 A55983	microtubule-associ
45	37	59.7	381	2 S51375	microtubule-associ

ALIGNMENTS

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RESULT 1
ORHUT2
Microtubule-associated protein tau, fetal (clone p18) - human
C:Species: Homo sapiens (man)
C>Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 02-Sep-1997
C:Accession: P00001
R:Lee, G.; Neve, R.L.; Kosik, K.S.
Neuron 2, 1615-1624, 1989
A:Title: The microtubule binding domain of tau protein.
A:Reference number: JN0009; MUID:90180482
A:Accession: P00001
A:Molecule type: mRNA
A:Residues: 1-316 <LDB>
A>Note: this sequence differs from a previously reported fetal tau protein sequence o
C:Genetics:
A:Gene: GDB:MAPT; MTBT1
A:Cross-references: GDB:119434; OMIM:157140
A:Map position: 17q21-17q21
C:Superfamily: microtubule-associated protein tau; MAP2/tau repeat homology
C:Keywords: alternative splicing; Alzheimer's disease; duplication; microtubule bindi
F:158-188/Domain: MAP2/tau repeat homology <MT1>
F:189-219/Domain: MAP2/tau repeat homology <MT2>
F:220-251/Domain: MAP2/tau repeat homology <MT3>

Query Match 93.5%; Score 58; DB 1; Length 316;
Best Local Similarity 83.3%; Pred. No. 0.02;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KSGYSXPGSPGT 12
DB 100 RSGYSSPGSPGT 111

RESULT 2
B28820
Microtubule-associated protein tau type 2 - mouse
C:Species: Mus musculus (house mouse)
C>Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 13-Aug-1999
C:Accession: B28820
R:Lee, G.; Cowan, N.; Kirschner, M.
Science 239, 285-288, 1988
A:Title: The primary structure and heterogeneity of tau protein from mouse brain.
A:Reference number: A94298; MUID:88099510
A:Accession: B28820
A:Molecule type: mRNA
A:Residues: 1-341 <LDB>
A:Cross-references: GB:M18775; NID:g201114; PTDN:AA40165.1; PTD:g201115
C:Superfamily: microtubule-associated protein tau; MAP2/tau repeat homology
C:Keywords: alternative splicing; microtubule binding; tandem repeat
F:183-213/Domain: MAP2/tau repeat homology <MT1>
F:214-244/Domain: MAP2/tau repeat homology <MT2>

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F:245-276/Domain: MAP2/tau repeat homology <MT3>

Query Match 93.5%; Score 58; DB 2; Length 341;
Best Local Similarity 83.3%; Pred. No. 0.022;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 KSGYSPGSPGT 12
Db 125 RSGYSPGSPGT 136

RESULT 3

A28820

Microtubule-associated protein tau type 1 - mouse

C:Species: Mus musculus (house mouse)

C:Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 13-Aug-1999

C:Accession: A28820

R:Lee, G.; Cowan, N.; Kirschner, M.

Science 239, 285-288, 1988

A:Title: The primary structure and heterogeneity of tau protein from mouse brain.

A:Reference number: A94298; MUID:88095510

A:Accession: A28820

A:Molecule type: mRNA

A:Residues: 1-364 <DE>

A:Cross-references: GB:M18776; NID:g201116; PIDN:AAA0166.1; PID:g201117

C:Superfamily: microtubule-associated protein tau; MAP2/tau repeat homology

C:Keywords: alternative splicing; microtubule binding; tandem repeat

F:183-213/Domain: MAP2/tau repeat homology <MT1>

F:214-244/Domain: MAP2/tau repeat homology <MT2>

F:245-276/Domain: MAP2/tau repeat homology <MT3>

Query Match 93.5%; Score 58; DB 2; Length 364;
Best Local Similarity 83.3%; Pred. No. 0.023;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 KSGYSPGSPGT 12
Db 125 RSGYSPGSPGT 136

RESULT 4

S46264

Microtubule-associated protein - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 13-Aug-1999

C:Accession: S46264

R:Sadot, E.; Marx, R.; Barg, J.; Behar, L.; Ginzburg, I.

J. Mol. Biol. 241, 325-331, 1994

A:Title: Complete sequence of 3'-untranslated region of tau from rat central nervous sys

A:Reference number: S46264; MUID:94334997

A:Accession: S46264

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-374 <SAD>

A:Cross-references: EMBL:X79321; NID:g517393; PIDN:CAA55889.1; PID:g517394

C:Superfamily: microtubule-associated protein tau; MAP2/tau repeat homology

F:185-215/Domain: MAP2/tau repeat homology <MT1>

F:216-246/Domain: MAP2/tau repeat homology <MT2>

F:247-277/Domain: MAP2/tau repeat homology <MT3>

F:278-309/Domain: MAP2/tau repeat homology <MT4>

Query Match 93.5%; Score 58; DB 2; Length 374;
Best Local Similarity 83.3%; Pred. No. 0.024;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 KSGYSPGSPGT 12
Db 127 RSGYSPGSPGT 138

RESULT 5

OR0072

Microtubule-associated protein tau, form 3 - bovine

N:Contains: microtubule-associated protein tau, form 4; microtubule-associated protel

C:Species: Bos primigenius taurus (cattle)

C:Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 31-Mar-1996

C:Accession: B31939; A48885; A28173

R:Himmler, A.; Drechsel, D.; Kirschner, M.W.; Martin Jr., D.W.

Mol. Cell. Biol. 9, 1381-1388, 1989

A:Title: Tau consists of a set of proteins with repeated C-terminal microtubule-bind

A:Reference number: A31939; MUID:89261765

A:Accession: B31939

A:Molecule type: mRNA

A:Residues: 1-402 <HM>

A:Cross-references: GB:M26157; GB:M26158

R:Pandel, H.K.; Lew, J.; Ali, Z.; Wang, J.H.

J. Biol. Chem. 268, 23512-23518, 1993

A:Title: Brain proline-directed protein kinase phosphorylates tau on sites that are a

A:Reference number: A48885; MUID:94043150

A:Accession: A48885

A:Molecule type: protein

A:Residues: 'X', 157-162, 'X', 164-165, 'X', 167-170, 192-195, 'X', 197-201, 'X', 358-364, 'X', 3

A:Experimental source: brain

A>Note: sequence modified after extraction from NCBI backbone

R:Alzawa, H.; Kawasaki, H.; Murofushi, H.; Kotani, S.; Suzuki, K.; Sakai, H.

J. Biol. Chem. 263, 7703-7707, 1988

A:Title: Microtubule-binding domain of Tau proteins.

A:Reference number: A28173; MUID:88227970

A:Accession: A28173

A:Molecule type: protein

A:Residues: 159-172, 'X', 174-177 <ATZ>

A:Experimental source: brain

C:Superfamily: microtubule-associated protein tau; MAP2/tau repeat homology

C:Keywords: alternative splicing; microtubule binding; phosphoprotein; tandem repeat

F:1-402/Product: microtubule-associated protein tau, form 3 #status predicted <BT4>

F:101-402/Product: microtubule-associated protein tau, form 5 #status predicted <BT7>

F:159-177/Region: microtubule binding #status experimental

F:213-243/Domain: MAP2/tau repeat homology <MT1>

F:244-274/Domain: MAP2/tau repeat homology <MT2>

F:275-305/Domain: MAP2/tau repeat homology <MT3>

F:306-337/Domain: MAP2/tau repeat homology <MT4>

F:156,163,196,202,365/Binding site: phosphate (Ser) (covalent) (by proline-directed k

F:166/Binding site: phosphate (Thr) (covalent) (by proline-directed kinase) #status p

Query Match 93.5%; Score 58; DB 1; Length 402;
Best Local Similarity 83.3%; Pred. No. 0.026;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 KSGYSPGSPGT 12
Db 155 RSGYSPGSPGT 166

RESULT 6

J50306

Microtubule-associated protein tau - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 31-Dec-1993

C:Accession: J50306; A33574

R:Kosik, K.S.; Orecchio, L.D.; Bakalis, S.; Neve, R.L.

Neuron 2, 1389-1397, 1989

A:Title: Developmentally regulated expression of specific tau sequences.

A:Reference number: J50306; MUID:90180457

A:Accession: J50306

A:Molecule type: mRNA

A:Residues: 1-432 <KOS>

A>Note: the sequence shown is from adult rat brain

A>Note: both fetal and adult forms were found in the paired helical filaments charact

R:Kanai, Y.; Takemura, R.; Oshima, T.; Mori, H.; Ihara, Y.; Yanagisawa, M.; Masaki, T

A>Title: Expression of multiple tau isoforms and microtubule bundle formation in fibrobl
A:Reference number: A33574; MID:89359509
A:Accession: A33574
A>Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-432 <RAN>
A>Note: A variant lacking residues 63-91 was also found
C:Superfamily: microtubule-associated protein tau; MAP2/tau repeat homology
C:Keywords: alternative splicing; Alzheimer's disease; calmodulin binding; microtubule b
F:743-773/Domain: MAP2/tau repeat homology <MT1>
F:774-304/Domain: MAP2/tau repeat homology <MT2>
F:305-335/Domain: MAP2/tau repeat homology <MT3>
F:336-367/Domain: MAP2/tau repeat homology <MT4>
F:382-313/disulfide bonds: status experimental
F:347/Binding site: phosphate (Ser) (covalent) status predicted

Query Match 93.5%; Score 58; DB 2; Length 432;
Best Local Similarity 83.3%; Pred. No. 0.028;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 KSGYXPGSPGT 12
DB 185 RSGYSPGSPGT 196

RESULT 7
ORF001
Microtubule-associated protein tau, long splice form - human
N:Alternate names: microtubule-binding protein tau; neurofibrillary tangle protein paire
N:Contains: microtubule-associated protein tau type II; microtubule-associated protein t
C:Species: Homo sapiens (man)
C:Date: 30-Jun-1990 #sequence_revision 03-May-1996 #text_change 22-Jun-1999
C:Accession: J030370; A30217; J00009; S03796; S26655; S26662; S17302; A43444; A27
R:Goedert, M.; Spillmann, M.G.; Jakes, R.; Rutherford, D.; Crowther, R.A.
Neuron 3, 519-526, 1989
A>Title: Multiple isoforms of human microtubule-associated protein tau: sequences and 1c
A:Reference number: J030370; MID:90380933
A:Accession: J030370
A:Molecule type: mRNA
A:Residues: 1-441 <GOE>
A>Note: six isoforms are found: the clone htau40 sequence is shown. Residues 45-73, 74-1
the clone htau4 sequence lacks inserts 1 and 2; the clone htau37 sequence lacks insert
R:Goedert, M.; Wischik, C.M.; Crowther, R.A.; Walker, J.E.; Klug, A.
Proc. Natl. Acad. Sci. U.S.A. 85, 4051-4055, 1988
A>Title: Cloning and sequencing of the cDNA encoding a core protein of the paired helica
A:Reference number: A30217; MID:88234557
A:Accession: A30217
A:Molecule type: mRNA
A:Residues: 1-44,103-274,306-441 <GO2>
A:Cross-references: GB:J03778; NID:9338684; PIDN:AAA60615.1; PID:9338685
R:Lee, G.; Neve, R.L.; Kosik, K.S.
Neuron 2, 1615-1624, 1989
A>Title: The microtubule binding domain of tau protein.
A:Reference number: J00009; MID:90180482
A:Accession: J00009
A:Molecule type: mRNA
A:Residues: 1-44,103-274,306-441 <LEE>
R:Goedert, M.; Spillmann, M.G.; Potler, M.C.; Ulrich, J.; Crowther, R.A.
EMBO J. 8, 393-399, 1989
A>Title: Cloning and sequencing of the cDNA encoding an isoform of microtubule-associated
A:Reference number: S03796; MID:89251564
A:Accession: S03796
A:Molecule type: mRNA
A:Residues: 1-44,103-441 <GO3>
A:Cross-references: EMBL:X14474; NID:936724; PIDN:CAA32636.1; PID:936725
R:Andreadis, A.; Brown, W.M.; Kosik, K.S.
Biochemistry 31, 10626-10633, 1992
A>Title: Structure and novel exons of the human tau gene.
A:Reference number: S26662; MID:93041757
A:Accession: S26665
A>Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA

A:Residues: 144-185 <AND>
A:Cross-references: EMBL:X61372; NID:936718; PID:936719
A>Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1991
A:Accession: S26666
A>Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 187-274 <AN2>
A:Cross-references: EMBL:X61374; NID:936722; PID:936723
A>Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1991
A:Accession: S26662
A:Molecule type: DNA
A:Residues: 371-441 <ANW>
A:Cross-references: EMBL:X61373
R:Jakes, R.; Novak, M.; Davison, M.; Wischik, C.M.
EMBO J. 10, 2725-2729, 1991
A>Title: Identification of 3- and 4-repeat tau isoforms within the PHF in Alzheimer's
A:Reference number: S17302; MID:92007714
A:Accession: S17302
A>Status: preliminary
A:Molecule type: protein
A:Residues: 268-274,306-395 <JAK>
R:Hasagawa, M.; Morishima-Kawashima, M.; Takio, K.; Suzuki, M.; Titani, K.; Ihara, Y.
J. Biol. Chem. 267, 17047-17054, 1992
A>Title: Protein sequence and mass spectrometric analyses of tau in the Alzheimer's d
A:Reference number: A43444; MID:92381012
A:Accession: A43444
A:Molecule type: protein
A:Residues: 2-73,103-130,151-180,191-254,260-269,275-290,299-317,322-340,344-347,354-
A:Residues: 2-73,103-130,151-180,191-254,260-269,275-290,299-317,322-340,344-347,354-
A:Experimental source: Alzheimer's disease; duplication; microtubule bindi
A>Note: sequence extracted from NCBI database (NCBI:112039)
C:Comment: This heterogeneous protein, which is found predominantly in cells of the n
O the core protein of the paired helical filament of Alzheimer's disease.
C:Genetics:
A:Gene: GDB:MAPT
A:Cross-references: GDB:119434; OMIM:157140
A:Map position: 17q21.1-17q21
C:Superfamily: microtubule-associated protein tau; MAP2/tau repeat homology
C:Keywords: alternative splicing; Alzheimer's disease; duplication; microtubule bindi
F:1-274,306-441/Product: microtubule-associated protein tau (clone htau39) #status pr
F:1-73,103-441/Product: microtubule-associated protein tau (clone htau3) #status pr
F:1-73,103-274,306-441/Product: microtubule-associated protein tau (clone htau37) #st
F:1-44,103-274,306-441/Product: microtubule-associated protein tau, fetal #status pre
F:1-44,103-441/Product: microtubule-associated protein tau type II #status predicted
F:252-282/Domain: MAP2/tau repeat homology <MT1>
F:283-313/Domain: MAP2/tau repeat homology <MT2>
F:314-344/Domain: MAP2/tau repeat homology <MT3>
F:345-376/Domain: MAP2/tau repeat homology <MT4>

Query Match 93.5%; Score 58; DB 1; Length 441;
Best Local Similarity 83.3%; Pred. No. 0.028;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 KSGYXPGSPGT 12
DB 194 RSGYSPGSPGT 205

RESULT 8
ORF001
Microtubule-associated protein tau, form 1 - bovine
N:Contains: microtubule-associated protein tau, form 2
C:Species: Bos primigenius taurus (cattle)
C:Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 22-Jun-1999
C:Accession: A31939; A33914; S04005; A48885; A28173; B33734
R:Himmler, A.; Drechsel, D.; Kirschner, M.W.; Martin Jr., D.W.
Mol. Cell. Biol. 9, 1381-1388, 1989
A>Title: Tau consists of a set of proteins with repeated C-terminal microtubule-bind
A:Reference number: A31939; MID:89261765
A:Accession: A31939
A:Molecule type: mRNA
A:Residues: 1-448 <RIM>

A:Cross-references: GB:M6157; NID:9514913; PIND:AAA30770.1; PID:9514914
R:Ripbal, K.; Grundke-Iqbal, I.; Smith, A.J.; George, L.; Tung, Y.C.; Zaidi, T.
Proc. Natl. Acad. Sci. U.S.A. 86, 5646-5650, 1989
A:Title: Identification and localization of a tau-peptide to paired helical filaments of
A:Reference number: A33914; MUID:89315854
A:Accession: A33914
A:Molecule type: protein
A:Residues: 28, 'A', 30-38, 'IG', 41, 'AP', 44, 'LK' <IOB>
A:Experimental source: brain
A:Note: 40-Pro was also found
R:Ripbal, K.; Smith, A.J.; Zaidi, T.; Grundke-Iqbal, I.
FEBS Lett. 248, 87-91, 1989
A:Title: Microtubule-associated protein tau. Identification of a novel peptide from bovin
A:Reference number: S04005; MUID:89252057
A:Accession: S04005
A:Molecule type: protein
A:Residues: 28, 'A', 30-38, 'IG', 41, 'AP', 44, 'LK' <IO2>
A:Experimental source: brain
A:Note: 40-Pro was also found
R:Ripbal, K.; Lew, J.; All, Z.; Wang, J.H.
J. Biol. Chem. 268, 23512-23518, 1993
A:Title: Brain proline-directed protein kinase phosphorylates tau on sites that are abn
A:Reference number: A48885; MUID:94043150
A:Accession: A48885
A:Molecule type: protein
A:Residues: 'X', 203-208, 'X', 210-211, 'X', 213-216, 238-241, 'X', 243-247, 'X', 404-410, 'X', 412-
A:Experimental source: brain
A:Note: sequence modified after extraction from NCBI backbone
R:Alalawa, H.; Kawasaki, H.; Murofushi, H.; Kotani, S.; Suzuki, K.; Sakai, H.
J. Biol. Chem. 263, 7703-7707, 1988
A:Title: Microtubule-binding domain of Tau proteins.
A:Reference number: A28173; MUID:88227970
A:Accession: A28173
A:Molecule type: protein
A:Residues: 205-218, 'X', 220-223 <AI2>
A:Experimental source: brain
C:Superfamily: microtubule-associated protein tau; MAP2/tau repeat homology
C:Keywords: alternative splicing; microtubule binding; phosphoprotein; tandem repeat
F:1-448/Product: microtubule-associated protein tau, form 1 #status predicted <Br43>
F:1-174, 193-448/Product: microtubule-associated protein tau, form 2 #status predicted <B
F:205-223/Region: microtubule binding #status experimental
F:259-289/Domain: MAP2/tau repeat homology <MT1>
F:290-330/Domain: MAP2/tau repeat homology <MT2>
F:332-351/Domain: MAP2/tau repeat homology <MT3>
F:352-383/Domain: MAP2/tau repeat homology <MT4>
F:202, 209, 242, 248, 411/Binding site: phosphate (Ser) (covalent) (by proline-directed kina
F:212/Binding site: phosphate (Thr) (covalent) (by proline-directed kinase) #status exp

Query Match 93.5%; Score 58; DB 1; Length 448;
Best Local Similarity 83.3%; Pred. NO. 0.029;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KSGYXPGSSPCT 12
:|||||
Db 201 RSGYSSPSSPCT 212

RESULT 9
A38235
microtubule-associated protein, 110K tau - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 31-Dec-1993 #sequence-revision 13-Dec-1993 #text-change 13-Aug-1999
C:Accession: A38235
R:Goedert, M.; Spillantini, M.G.; Crowther, R.A.
Proc. Natl. Acad. Sci. U.S.A. 89, 1983-1987, 1992
A:Title: Cloning of a big tau microtubule-associated protein characteristic of the perip
A:Reference number: A38235; MUID:92179305
A:Accession: A38235
A:Molecule type: mRNA
A:Residues: 1-686 <GOE>
A:Cross-references: GB:M64156; NID:g207157; PIND:AAA42204.1; PID:g207158
A:Note: sequence extracted from NCBI backbone (NCBIN:87358, NCBIIP:87355)

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C:Superfamily: microtubule-associated protein tau; MAP2/tau repeat homology
C:Keywords: alternative splicing; microtubule binding; tandem repeat
F:/497-527/Domain: MAP2/tau repeat homology <MT1>
F:/528-536/Domain: MAP2/tau repeat homology <MT2>
F:/559-589/Domain: MAP2/tau repeat homology <MT3>
F:/590-621/Domain: MAP2/tau repeat homology <MT4>

Query Match      93.5%; Score 58; DB 2; Length 686;
Best Local Similarity 83.3%; Pred. No. 0.044;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 KSGYSXPGSPGT 12
          :|||||
Db       439 RSGYSSPSPGPT 450

RESULT 10
A:Accession: A45301
microtubule-associated protein tau - mouse
N:Alternate names: microtubule binding protein tau
C:Species: Mus musculus (house mouse)
C:Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 13-Aug-1999
C:Accession: A45301; S31658
R:Couchie, D.; Matilla, C.; Georgiev, I.S.; Ilem, R.K.; Shelanski, M.L.; Nunez, J.
Proc. Natl. Acad. Sci. U.S.A. 89, 4378-4381, 1992
A>Title: Primary structure of high molecular weight tau present in the peripheral ner
A:Reference number: A45301; MUID:92262443
A:Accession: A45301
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-733 <CDU>
A>Note: This sequence is inconsistent with the nucleotide translation
A:Note: sequence extracted from NCBI backbone (NCBIN:102045, NCBIP:102046)
R:Kerner, L.; Fortner, M.; Hutter, H.; Hoefler, G.; Kurzbauner, R.; Zatloukal, R.; Kr
submitted to the EMBL Data Library, May 1992
A:Description: First observation of mRNA for a tau-protein from murine liver and kidney
A:Reference number: S31658
A:Accession: S31658
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-733 <KEND>
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-733 <KEND>
A:Cross-references: EMBL:Z12133; NID:g54263; PIDN:CAAT8121.1; PID:g388534
C:Superfamily: microtubule-associated protein tau; MAP2/tau repeat homology
C:Keywords: microtubule binding; tandem repeat
F:/544-574/Domain: MAP2/tau repeat homology <MT1>
F:/575-605/Domain: MAP2/tau repeat homology <MT2>
F:/606-636/Domain: MAP2/tau repeat homology <MT3>
F:/637-668/Domain: MAP2/tau repeat homology <MT4>

Query Match      93.5%; Score 58; DB 2; Length 733;
Best Local Similarity 83.3%; Pred. No. 0.047;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 KSGYSXPGSPGT 12
          :|||||
Db       486 RSGYSSPSPGPT 497

RESULT 11
A:Accession: T19220
hypothetical protein ClD8.8 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jan-2000
C:Accession: T19220
R:McMurray, A.
submitted to the EMBL Data Library, June 1996
A:Reference number: Z19092
A:Accession: T19220
A>Status: preliminary; translated from GB/EMBL/DDJ
A:Molecule type: DNA
A:Residues: 1-295 <WTL>

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A:Cross-references: EMBL:Z73969; PIDN:CAA98236.1; GSPDB:GN00023; CESP:C12D8.8
 A:Experimental source: clone C12D8
 C:Genetics:
 A:Gene: CESP:C12D8.8
 A:Map position: 5
 A:Introns: 39/3
 C:Superfamily: unassigned collagens

Query Match 71.0%; Score 44; DB 2; Length 295;
 Best Local Similarity 63.6%; Pred. No. 3.9;
 Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 KSGYXPGSPG 11
 ||| |||
 DB 213 KRGYAGAPG 223

RESULT 12

T45928
 reductase-like protein - Arabidopsis thaliana
 N:Alternate names: protein F5K20.180
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C>Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 18-Feb-2000
 C:Accession: T45928
 R:Konfort, A.; Casacuberta, E.; Puigdomenech, P.; Meyers, H.W.; Lemcke, K.; Mayer, K.F.X.
 submitted to the Protein Sequence Database, January 2000
 A:Reference number: Z23017
 A:Accession: T45928
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-315 <MON>
 A:Cross-references: EMBL:A1132960
 A:Experimental source: cultivar Columbia; BAC clone F5K20
 C:Genetics:
 A:Map position: 3
 A:Introns: 40/3; 57/3; 83/2; 112/3; 204/3; 287/3
 A:Note: F5K20.180
 C:Superfamily: aldehyde reductase

Query Match 71.0%; Score 44; DB 2; Length 315;
 Best Local Similarity 81.8%; Pred. No. 4.2;
 Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 SGYXPGSPGT 12
 ||| |||
 DB 204 SGYSPGSPGT 214

RESULT 13

A75621
 TorS-related protein - Deinococcus radiodurans (strain R1)
 C:Species: Deinococcus radiodurans
 C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000
 C:Accession: A75621
 R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
 M.; Shen, M.; Vamthyan, J.J.; Lam, P.; McDonald, L.; Uterback, T.; Zalewski, C.; Ma
 S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
 Science 286, 1571-1577, 1999
 A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
 A:Reference number: A75550; MIMD:20056896
 A:Accession: A75621
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-351 <WHI>
 A:Cross-references: GB:AE001826; NID:g6460827; PIDN:AAJ12581.1; PID:g6460877; TRIR:DRB00
 A:Experimental source: strain R1
 C:Genetics:
 A:Gene: DRB0027
 A:Map position: megaplasmid
 A:Genome: plasmid
 A:Note: plasmid MPI

Query Match 69.4%; Score 43; DB 2; Length 351;
 Best Local Similarity 58.3%; Pred. No. 6.8;
 Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 1 KSGYXPGSPGT 12
 ||| |||
 DB 92 RCGYTAGTPT 103

RESULT 14

T19894
 hypothetical protein C41G7.3 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
 C:Accession: T19894
 R:Steward, C.
 submitted to the EMBL Data Library, October 1996
 A:Reference number: Z19192
 A:Accession: T19894
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-553 <MTL>
 A:Cross-references: EMBL:Z81048; PIDN:CAB02840.1; GSPDB:GN00019; CESP:C41G7.3
 A:Experimental source: clone C41G7
 C:Genetics:
 A:Gene: CESP:C41G7.3
 A:Map position: 1
 A:Introns: 25/1; 81/2; 106/3; 157/1; 179/3; 245/3; 368/1; 389/3; 423/3; 517/3

Query Match 69.4%; Score 43; DB 2; Length 553;
 Best Local Similarity 72.7%; Pred. No. 11;
 Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 2 SGYXPGSPGT 12
 ||| |||
 DB 323 SGYSTPGSPGT 333

RESULT 15

S28353
 probable polyketide synthase - Emericella nidulans
 C:Species: Emericella nidulans, Aspergillus nidulans
 C>Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 12-Feb-1999
 C:Accession: S28353
 R:Mayorga, M.E.; Timberlake, W.E.
 Mol. Gen. Genet. 235, 205-212, 1992
 A:Title: The developmentally regulated Aspergillus nidulans wa gene encodes a polypep
 A:Reference number: S28353; MIMD:93101122
 A:Accession: S28353
 A:Molecule type: DNA
 A:Residues: 1-1986 <MAV>
 A:Cross-references: EMBL:X65866; NID:g5508; PID:g5509
 C:Genetics:
 A:Gene: WA
 A:Introns: 96/2; 193/3; 1336/3; 1586/3
 C:Superfamily: 3-oxoacyl-[acyl-carrier-protein] synthase I homology; acyl carrier pro
 F:397-805/Domain: 3-oxoacyl-[acyl-carrier-protein] synthase I homology <OAS>
 F:111-119/Domain: [acyl-carrier-protein] S-malonyltransferase homology <AMT>
 F:1648-1118/Domain: acyl carrier protein homology <ACP>
 F:1766-1840/Domain: acyl carrier protein homology <ACPL>

Query Match 67.7%; Score 42; DB 2; Length 1986;
 Best Local Similarity 72.7%; Pred. No. 56;
 Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 2 SGYXPGSPGT 12
 ||| |||
 DB 1746 SGYSPGSPGT 1756

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Job time: 1983 sec
